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Set	Items	Description
S1	44	PORPHYRA AND CYTOCHROME
S2	13	S1 AND TENERA
S3	15	S1 AND (CYTOCHROME()C)
S4	4	S3 AND TENERA
S5	4	PORPHYRA AND (CYTOCHROME()C6)

? t s1/7/1-44

1/7/1
DIALOG(R)File 5:Biosis Previews(R)

19256073 BIOSIS NO.: 200600601468
Assessing the use of the mitochondrial cox1 marker for use in DNA barcoding of red algae (Rhodophyta)
AUTHOR: Robba Lavinia; Russell Stephen J; Barker Gary L; Brodie Juliet (Reprint)
AUTHOR ADDRESS: Nat Hist Museum, Dept Bot, Cromwell Rd, London SW7 5BD, UK **UK
AUTHOR E-MAIL ADDRESS: J.Brodie@nhm.ac.uk
JOURNAL: American Journal of Botany 93 (8): p1101-1108 AUG 2006 2006
ISSN: 0002-9122
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The red algae, a remarkably diverse group of organisms, are difficult to identify using morphology alone. Following the proposal to use the mitochondrial %%%cytochrome%%% c oxidase subunit 1 (cox1) for DNA barcoding animals, we assessed the use of this, ne in the identification of red algae using 48 samples plus 31 sequences obtained from GenBank. The data set spanned six gene orders of red algae: the Bangiales, Ceramiales, Corallinales, Gigartinales, Gracilariales and Rhodymeniales. The results indicated that species could be discriminated. Intraspecific variation was between 0 and 4 bp over 539 bp analyzed except in Mastocarpus stellatus (0-14 bp) and Gracilaria gracilis (0-11 bp). Cryptic diversity was found in Bangia fuscopurpurea, Corallina officinalis, G. gracilis, M. stellatus, %%%Porphyra%%% leucosticta and P. umbilicalis. Interspecific variation across all taxa was between 28 and 148 bp, except for G. gracilis and M. stellatus. A comparison of cox1 with the plastid Rubisco spacer for %%%Porphyra%%% species revealed that it was a more sensitive marker in revealing incipient speciation and cryptic diversity. The cox1 gene has the potential to be used for DNA barcoding of red algae, although a good taxonomic foundation coupled with extensive sampling of taxa is essential for the development of an effective identification system.

1/7/2
DIALOG(R)File 5:Biosis Previews(R)

18033493 BIOSIS NO.: 200400404282
Bioinformatics studies on photosynthetic system genes in cyanobacteria and chloroplasts
AUTHOR: Shi Ding-Ji (Reprint); Zhang Chao; Li Shi-Ming; Li Ci-Shan; Zhang Peng-Peng; Yang Ming-Li
AUTHOR ADDRESS: Coll Marine Sci and Engn, Tianjin Univ Sci and Technol, Tianjin, 300450, China**China
AUTHOR E-MAIL ADDRESS: cyanoshi@public.bta.net.cn
JOURNAL: Acta Genetica Sinica 31 (6): p627-633 June 2004 2004
MEDIUM: print
ISSN: 0379-4172 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Chinese

ABSTRACT: This study compared homology of base sequences in genes encoding photosynthetic system proteins of cyanobacteria (Synechocystics sp. PCC6803, Nostoc sp. PCC7120) with these of chloroplasts (from Marchantia Polymorpha, Nicotiana tobacum, Oryza sativ, Euglena gracilis, Pinus thunbergii, Zea mays, Odentella sinesis, Cyanophora paradoxa, %%%Porphyra%%% purpurea and Arabidopsis thaliana) by BLAST method. While the gene sequence of Synechocystics sp. PCC6803 was considered as the criterion (100%) the homology of others were compared with it. Among the genes for photosystem I psaC homology was the highest (90.14%) and the lowest was psaJ (52.24%). The highest ones were psbD (83.71%) for photosystem II, atpB (79.58%) for ATP synthase and petB (81.66%) for %%%cytochrome%%% b6/f complex. The lowest ones were psbN (49.70%) for photosystem II, atpF (26.69%) for ATP synthase and petA (55.27%) for %%%cytochrome%%% b6/f complex. Also, this paper discussed why the homology of gene sequences was the highest or the lowest. No report has been published and this bioinformatics research may provide some evidences for the origin and evolution of chloroplasts.

1/7/3
DIALOG(R)File 5:Biosis Previews(R)

17041661 BIOSIS NO.: 200300000380
Increasing the conformational stability by replacement of heme axial ligand in c-type %%%cytochrome%%%.
AUTHOR: Satoh Tadashi; Itoga Akito; Isogai Yasuhiro; Kurihara Masaaki; Yamada Seiji; Natori Miwa; Suzuki Noriko; Suruga Kohei; Kawachi Ryu; Arahira Masaomi; Nishio Toshiyuki; Fukazawa Chikafusa; Oku Tadatake (Reprint)
AUTHOR ADDRESS: Department of Biological Chemistry, College of Bioresource Sciences, Nihon University, Kameino 1866, Fujisawa, Kanagawa, 252-8510, Japan**Japan
AUTHOR E-MAIL ADDRESS: oku@brs.nihon-u.ac.jp
JOURNAL: FEBS Letters 531 (3): p543-547 20 November, 2002 2002
MEDIUM: print
ISSN: 0014-5793
DOCUMENT TYPE: Article

RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: To investigate the role of the heme axial ligand in the conformational stability of c-type %%%cytochrome%%%, we constructed M58C and M58H mutants of the red alga %%%Porphyra%%% yezoensis %%%cytochrome%%% c6 in which the sixth heme iron ligand (Met58) was replaced with Cys and His residues, respectively. The Gibbs free energy change for unfolding of the M58H mutant in water (DELTAGdegreeunf =1.48 kcal/mol) was lower than that of the wild-type (2.43 kcal/mol), possibly due to the steric effects of the mutation on the apoprotein structure. On the other hand, the M58C mutant exhibited a DELTAGdegreeunf of 5.45 kcal/mol, a significant increase by 3.02 kcal/mol compared with that of wild-type. This increase was possibly responsible for the sixth heme axial bond of M58C mutant being more stable than that of wild-type according to the heme-bound denaturation curve. Based on these observations, we propose that the sixth heme axial ligand is an important key to determine the conformational stability of c-type cytochromes, and the sixth Cys heme ligand will give stabilizing effects.

1/7/4
DIALOG(R)File 5:Biosis Previews(R)

15978829 BIOSIS NO.: 200100150668
Fatty acid oxidizing activity in a red marine alga, %%%Porphyra%%% sp
AUTHOR: Kajiwara Tadahiko (Reprint); Matsui Kenji; Akakabe Yoshihiko; Okajima Kaori; Chirapart Anong
AUTHOR ADDRESS: Department of Biological Chemistry, Faculty of Agriculture, Yamaguchi University, Yamaguchi, 753-8515, Japan**Japan
JOURNAL: Zeitschrift fuer Naturforschung Section C Journal of Biosciences 55 (11-12): p903-909 November-December, 2000 2000
MEDIUM: print
ISSN: 0939-5075
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A crude enzyme solution prepared from fronds of %%%Porphyra%%% sp. showed remarkable oxygen uptake activity when linoleic acid was added as a substrate. Fatty acid oxidizing activity was mainly present in the soluble fraction of the crude homogenate. The activity was purified 769-fold from mature fronds by ammonium sulfate fractionation, ion-exchange and hydrophobic chromatography. SDS-PAGE analysis of the purified proteins indicated that its subunit size was about 13 kDa. Gel filtration chromatography equipped with a photodiode array detector revealed that the activity was associated with a protein having a molecular weight of 12,500-13,000. It eluted with a chromophore having the maximum absorbance at 417 nm, thus, the protein was suggested to be a heme protein. The spectrophotometric property of the protein was highly similar to that of %%%cytochrome%%% c suggesting that it has heme c as a prosthetic group. The protein showed highest oxygenation activity against linoleic acid, and alpha-linolenic acid and arachidonic acid followed, but oleic acid could not be oxidized. From linoleic acid the protein formed 9- and 13-hydroperoxides to the same extent, and both were shown to be racemic. These results showed that the oxidizing activity is

accountable to a %%%cytochrome%%%, but not to a typical lipoxygenase.

1/7/5
DIALOG(R)File 5:Biosis Previews(R)

15877512 BIOSIS NO.: 200100049351
Structure of %%%cytochrome%%% c6 from the red alga %%%Porphyra%%% yezoensis at 1.57 ANG resolution
AUTHOR: Yamada Seiji; Park Sam-Yong; Shimizu Hideaki; Koshizuka Yasutaka; Kadokura Kazunari; Satoh Tadashi; Suruga Kohei; Ogawa Masahiro; Isogai Yasuhiro; Nishio Toshiyuki; Shiro Yoshitsugu; Oku Tadatake (Reprint)
AUTHOR ADDRESS: Department of Biological Chemistry, College of Bioresource Sciences, Nihon University, 1866 Kameino, Fujisawa, Kanagawa, 252-8510, Japan**Japan
JOURNAL: Acta Crystallographica Section D Biological Crystallography 56 (12): p1577-1582 December, 2000 2000
MEDIUM: print
ISSN: 0907-4449
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The crystal structure of %%%cytochrome%%% c6 from the red alga %%%Porphyra%%% yezoensis has been determined at 1.57 ANG resolution. The crystal is tetragonal and belongs to space group P43212, with unit-cell parameters a = b = 49.26 (3), c = 83.45 (4) ANG and one molecule per asymmetric unit. The structure was solved by the molecular-replacement method and refined with X-PLOR to an R factor of 19.9% and a free R factor of 25.4%. The overall structure of %%%cytochrome%%% c6 follows the topology of class I c-type cytochromes in which the heme prosthetic group covalently binds to Cys14 and Cys17, and the iron has an octahedral coordination with His18 and Met58 as the axial ligands. The sequence and the structure of the eukaryotic red algal %%%cytochrome%%% c6 are very similar to those of a prokaryotic cyanobacterial %%%cytochrome%%% c6 rather than those of eukaryotic green algal c6 cytochromes.

1/7/6
DIALOG(R)File 5:Biosis Previews(R)

15369869 BIOSIS NO.: 200000088182
Crystallization and preliminary X-ray diffraction studies of %%%cytochrome%%% c6 from %%%Porphyra%%% yezoensis
AUTHOR: Sasaki Tomokazu; Nakahara Megumi; Matsuda Aya; Yamasaki Takenobu; Katoh Sakae; Ohshima Shigeru; Oonishi Isao; Uchida Akira (Reprint)
AUTHOR ADDRESS: Department of Biomolecular Science, Toho University, Miyama 2-2-1, Funabashi, Chiba, 274-8510, Japan**Japan
JOURNAL: Acta Crystallographica Section D Biological Crystallography 56 (1): p79-80 Jan., 2000 2000
MEDIUM: print
ISSN: 0907-4449
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: %%%Cytochrome%%% c6 from the red alga. %%%Porphyra%%% yezoensis has been purified and crystallized by the sitting-drop vapour-diffusion method. Two different crystal forms, tetragonal and orthorhombic, were obtained. The tetragonal crystals belong to space group P41212 or P43212, with unit-cell dimensions a = 49.33 (2), c = 83.70 (10) ANG. The orthorhombic crystals belong to space group P212121, with unit-cell dimensions a = 46.74 (2), b = 49.42 (1), c = 37.11 (1) ANG. Absorption spectra of the crystals showed that the tetragonal form was oxidized and the orthorhombic form was reduced.

1/7/7
DIALOG(R)File 5:Biosis Previews(R)

14812605 BIOSIS NO.: 199900072265
Characterization of the PetM subunit of the b6f complex from higher plants
AUTHOR: Kuegler Marion; Kruft Volker; Schmitz Udo K; Braun Hans-Peter (Reprint)
AUTHOR ADDRESS: Inst. Angewandte Genet., Univ. Hannover, Herrenhaeuser Str. 2, 30419 Hannover, Germany**Germany
JOURNAL: Journal of Plant Physiology 153 (5-6): p581-586 Nov., 1998 1998
MEDIUM: print
ISSN: 0176-1617
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The chloroplast %%%cytochrome%%% b6f complex comprises seven subunits, three of which - designated the PetG, PetL and PetM proteins - are very small. To determine structural data on the PetM protein from higher plants the spinach b6f complex was isolated by a novel isolation procedure based on blue native polyacrylamide gel electrophoresis (BN-PAGE). Starting with only 30 mg of chloroplast protein the enzyme complex is obtained in very pure form as demonstrated by analysis with Tricine-SDS/PAGE. The primary structure of the PetM subunit was investigated by direct amino acid sequencing and by sequencing of a corresponding cDNA clone from Arabidopsis thaliana. Arabidopsis PetM comprises 40 amino acids and is synthesized with a N-terminal extension of 56 amino acids that resembles stroma-targeting peptides. Hence, the PetM protein is assumed to be nuclear encoded and posttranslationally imported into chloroplasts. Arabidopsis PetM exhibits 58% sequence identity with PetM from Chlamydomonas. Furthermore, Arabidopsis PetM resembles the deduced amino acid sequences of small organelle-encoded open reading frames of the red alga %%%Porphyra%%% purpurea, the diatom Odontella sinensis, the green alga Cyanophora paradoxa and the cyanobacterium Synechocystis. The primary structure of PetM does not show any significant sequence similarity to the sequences of one of the small subunits of the mitochondrial bc1 complex. The overall subunit compositions of chloroplastt b6f complexes and mitochondrial bc1 complexes are compared and discussed.

1/7/8
DIALOG(R)File 5:Biosis Previews(R)

14283445 BIOSIS NO.: 199800077692
Ccs1, a nuclear gene required for the post-translational assembly of chloroplast c-type cytochromes
AUTHOR: Inoue Kairo; Dreyfuss Beth Welty; Kindle Karen L; Stern David B; Merchant Sabeeha; Sodeinde Ola A (Reprint)
AUTHOR ADDRESS: Dep. Biochem. Mol. Biol., Pennsylvania State Univ., University Park, PA 16802, USA**USA
JOURNAL: Journal of Biological Chemistry 272 (50): p31747-31754 Dec. 12, 1997 1997
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Nuclear genes play important regulatory roles in the biogenesis of the photosynthetic apparatus of eukaryotic cells by encoding factors that control steps ranging from chloroplast gene transcription to post-translational processes. However, the identities of these genes and the mechanisms by which they govern these processes are largely unknown. By using glass bead-mediated transformation to generate insertional mutations in the nuclear genome of Chlamydomonas reinhardtii, we have generated four mutants that are defective in the accumulation of the %%%cytochrome%%% b6f complex. One of them, strain abf3, also fails to accumulate holocytochrome c6. We have isolated a gene, Ccs1, from a C. reinhardtii genomic library that complements both the %%%cytochrome%%% b6f and %%%cytochrome%%% c6 deficiencies in abf3. The predicted protein product displays significant identity with Ycf44 from the brown alga Odontella sinensis, the red alga %%%Porphyra%%% purpurea, and the cyanobacterium Synechocystis strain PCC 6803 (25-33% identity). In addition, we note limited sequence similarity with ResB of Bacillus subtilis and an open reading frame in a homologous operon in Mycobacterium leprae (11-12% identity). On the basis of the pleiotropic c-type %%%cytochrome%%% deficiency in the ccs1 mutant, the predicted plastid localization of the protein, and its relationship to candidate %%%cytochrome%%% biosynthesis proteins in Gram-positive bacteria, we conclude that Ccs1 encodes a protein that is required for chloroplast c-type holocytochrome formation.

1/7/9
DIALOG(R)File 5:Biosis Previews(R)

14205432 BIOSIS NO.: 199799839492
Cloning and sequence of a complementary DNA for red alga %%%cytochrome%%% f as a NO scavenger
AUTHOR: Kadokura Kazunari (Reprint); Yamada Seiji (Reprint); Saito Hiroko (Reprint); Nishio Toshiyuki (Reprint); Fukazawa Chikafusa; Oku Tadatake (Reprint)
AUTHOR ADDRESS: Dep. Biological Chem., Coll. Bioresource Sci., Nihon Univ., Setagaya, Tokyo, 154, Japan**Japan
JOURNAL: Japanese Journal of Pharmacology 75 (SUPPL. 1): p113P 1997 1997
CONFERENCE/MEETING: 5th International Meeting on the Biology of Nitric Oxide Kyoto, Japan September 15-19, 1997; 19970915
ISSN: 0021-5198

DOCUMENT TYPE: Meeting; Meeting Abstract; Meeting Poster
RECORD TYPE: Citation
LANGUAGE: English

1/7/10
DIALOG(R)File 5:Biosis Previews(R)

12059541 BIOSIS NO.: 199497080826
Purification and properties of NADH:nitrate reductase from the red alga %%%Porphyra%%% yezoensis
AUTHOR: Nakamura Yoshiko; Ikawa Tomoyoshi
AUTHOR ADDRESS: Inst. Biol. Sci., Univ. Tsukuba, Tsukuba, Ibaraki 305, Japan**Japan
JOURNAL: Plant and Cell Physiology 34 (8): p1239-1249 1993 1993
ISSN: 0032-0781
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Assimilatory nitrate reductase (NADH) (EC 1.6.6. 1) from the red alga %%%Porphyra%%% yezoensis was purified 5,700-fold by a combination of polyethylene glycol (PEG) treatment, ammonium sulfate fractionation, chromatography on columns of butyl-Toyopearl 650-M, Blue Sepharose CL-6B, DEAE-cellulose (DE 52), and hydroxyapatite, gel filtration on Sephacryl S-400. The purest preparation of the enzyme had a specific activity of 12.5 units mg-1 protein. A single band of protein was detected after polyacrylamide gel electrophoresis under nondenaturing conditions. This band corresponded to a band that stained positive for reduced methyl viologen-nitrate reductase activity. The molecular weight of the native enzyme was estimated to be 220,000. A single band of a protein with a molecular weight of 100,000 was detected after sodium dodecyl sulfate-polyacrylamide gel electrophoresis. These results indicate that the native nitrate reductase is composed of two identical subunits. The homogeneous preparation of nitrate reductase had a UV/visible spectrum typical of a b-type %%%cytochrome%%%. The K-m values for NADH and KNO-3 were 23 mu-M and 64 mu-M, respectively. The pH optimum for the reaction catalyzed by the nitrate reductase was 8.3, while pH values that supported maximum partial activities ranged from 7.0 to 8.5. Sulfhydryl reagents, such as p-HMB and NEM, inhibited full and NADH-utilizing partial activities, while cyanide and azide were effective inhibitors of full and nitrate-reducing partial activities.

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DIALOG(R)File 5:Biosis Previews(R)

11892222 BIOSIS NO.: 199396056638
Selective extraction of 22 kDA and 10 kDa polypeptides from Photosystem II without removal of 23 kDa and 17 kDa extrinsic proteins
AUTHOR: Mishra Ranjit K; Ghanotakis Demetrios F (Reprint)
AUTHOR ADDRESS: Dep. Chem., Univ. Crete, P.O. Box 1470, 71 409 Iraklion, Crete, Greece**Greece
JOURNAL: Photosynthesis Research 36 (1): p11-16 1993
ISSN: 0166-8595

DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Selective solubilization of Photosystem Ii membranes with the non-ionic detergent octyl thioglucopyranoside has allowed the isolation of a PS II system which has been depleted of the 22 and 10 kDa polypeptides but retains all three extrinsic proteins (33, 23 and 17 kDa). The PS II membranes which have been depleted of the 22 and 10 kDa species show high rates of oxygen evolution activity, external calcium is not required for activity and the manganese complex is not destroyed by exogenous reductants. When we compared this system to control PS II membranes, we observed a minor modification of the reducing side, and a conversion of the high-potential to the low-potential form of %%%cytochrome%%% b-559.

1/7/12
DIALOG(R)File 5:Biosis Previews(R)

11202703 BIOSIS NO.: 199293045594
BIOSYNTHESIS OF PHYCOBILINS FERREDOXIN-MEDIATED REDUCTION OF BILIVERDIN CATALYZED BY EXTRACTS OF CYANIDIUM-CALDARIUM
AUTHOR: BEALE S I (Reprint); CORNEJO J
AUTHOR ADDRESS: DIV BIOL MED, BROWN UNIV, PROVIDENCE, RHODE ISLAND 02912, USA**USA
JOURNAL: Journal of Biological Chemistry 266 (33): p22328-22332 1991
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Cell-free extract of the unicellular rhodophyte, Cyanidium caldarium catalyzes enzymatic reduction of biliverdin IX.alpha. to phycocyanobilin, the chromophore of the light-harvesting phycobiliprotein, phycocyanin. The enzyme activity is soluble, and the required reductant is NADPH. The extract has been separated into three protein fractions, all of which are required to reconstitute biliverdin reduction. One fraction contains ferredoxin, which was identified by its adsorption spectrum. This fraction could be replaced with commercial ferredoxin derived from spinach or the red alga, %%%Porphyra%%% umbilicalis. The second protein fraction contains ferredoxin-NADP+ reductase, which was identified by the ability to catalyze ferredoxin-dependent reduction of %%%cytochrome%%% c in the presence of NADPH. This fraction could be replaced with commercial spinach ferredoxin-NADP+ reductase. These two components appear to be identical to previously described components of the algal heme oxygenase system that catalyzes biliverdin IX.alpha. formation from protoheme in C. caldarium extracts. The third protein fraction, in the presence of the first two (or their commercial counterparts) plus NADPH, catalyzes the reduction of biliverdin IX.alpha. to phycocyanobilin. The results indicate that the transformation of biliverdin to phycocyanobilin catalyzed by C. caldarium extracts is a ferredoxin-linked reduction process. The results also suggest the possibility that heme oxygenation and biliverdin reduction may occur in C. caldarium on associated enzyme systems.

1/7/13
DIALOG(R)File 5:Biosis Previews(R)

11166858 BIOSIS NO.: 199293009749
%%%CYTOCHROME%%% C-553 FROM TWO SPECIES OF MACROALGAE
AUTHOR: PRICE N T (Reprint); SMITH A J; SYKES A G; ROGERS L J
AUTHOR ADDRESS: DEP BIOCHEMISTRY, UNIVERSITY COLLEGE WALES, ABERYSTWYTH, DYFED SY23 3DD, UK**UK
JOURNAL: Phytochemistry (Oxford) 30 (9): p2845-2848 1991
ISSN: 0031-9422
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: %%%Cytochrome%%% c-553 has been purified to homogeneity from the red macroalgae Chondrus crispus and %%%Porphyra%%% umbilicalis. Whereas Prophyra umbilicalis possessed a single %%%cytochrome%%% c-553, isoforms of the %%%cytochrome%%% in approximate ratio 4:1 were found in Chondrus crispus. The Mr of all the cytochromes was 12 000 as measured by SDS-PAGE. The absorption spectrum of the reduced %%%cytochrome%%% showed maxima at 270-272 nm (protein), 414-416 nm (.gamma.-peak), 522 nm (.beta.-peak) and 553 nm (.alpha.-peak) and molar extinction coefficients were consistent with single haem per molecule. The .gamma. to .alpha. absorption ratio was close to 7.0 for the %%%Porphyra%%% umbilicalis %%%cytochrome%%% and Chondrus crispus major %%%cytochrome%%%. Reduced-oxidised difference spectra were closely similar. The midpoint redox potentials of the one-electron transfers were +340 mV for the %%%Porphyra%%% umbilicalis %%%cytochrome%%% c-553, and +330 and +285 mV for the major and minor isoforms of Chondrus crispus. While the cytochromes of highest redox potential are presumed to be implicated in photosynthetic electron transport in place of plastocyanin, which these algae apparently lack, the metabolic role for the Chondrus crispus minor %%%cytochrome%%% c-553 is enigmatic.

1/7/14
DIALOG(R)File 5:Biosis Previews(R)

10213357 BIOSIS NO.: 199089131248
CHANGES IN THE PHOTOSYNTHETIC APPARATUS OF RED ALGAE INDUCED BY SPECTRAL ALTERATION OF THE LIGHT FIELD II. FURTHER CHARACTERIZATION OF THE LIGHT-DEPENDENT REGULATION OF THE APPARENT QUANTUM YIELD OF PS I
AUTHOR: REHM A M (Reprint); GUELZOW M; MARQUARDT J; RIED A
AUTHOR ADDRESS: BOTANISHCHES INST, J W GOETHE UNIV, SIESMAYERSTRASSE 70, D-6000 FRANKFURT AM MAIN, FRG**WEST GERMANY
JOURNAL: Biochimica et Biophysica Acta 1016 (1): p127-136 1990
ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Several red algae show a light-dependent regulation of the apparent quantum yield of PS I (Rehm, A.M., Gulzow, M. and Ried, A.

(1989) Biochim. Biophys. Acta 973, 131-137). The induction of a reduced quantum yield of PS I by light 1 (L1) (exciting preferably chlorophyll) and its revision either in L2 (exciting the phycobiliproteins) or in darkness show different characteristics in %%%Porphyra%%% yezoensis, Rhodella violacea and Porphyridium purpureum. The process of induction, however, is always faster than its reversion. The ability to regulate the quantum yield of PS I is strongly influenced by temperature, not by NH4Cl. The 77 K fluorescence spectra of PS I in L1 (452 nm) do not show differences after pretreatment in L1, L2 or darkness which could be correlated with an altered quantum yield of PS I. Also, the wavelength of the actinic L1 (694-720 nm) has no influence on the observable differences in P-700 and %%%cytochrome%%% f oxidation after preillumination with L1 or L2. These data are interpreted as evidence against a possible decrease of the apparent quantum yield of PS I as a consequence of a functional decoupling of antenna and reaction center of PS I. The fact that in thylakoids the addition of ascorbate (2-10 mM) largely protects from a reduction of the apparent quantum yield of PS I by L1 preillumination and the clear dependence of the PS I activity upon the redox potential of the medium indicates a control of the quantum yield of PS I by a thylakoidal redox component accessible to external redox components. The redox midpoint potential of this component is +140 mV at pH 7.8. This redox center does not participate in linear electron transport between the photosystems and is located nearby PS I.

09660601 BIOSIS NO.: 198987108492
CHANGES IN THE PHOTOSYNTHETIC APPARATUS OF RED ALGAE INDUCED BY SPECTRAL ALTERATION OF THE LIGHT FIELD I. A DECREASE IN THE APPARENT QUANTUM YIELD OF PS I CAUSED BY PREILLUMINATION WITH LIGHT 1
AUTHOR: REHM A M (Reprint); GUELZOW M; RIED A
AUTHOR ADDRESS: BOTANISCHES INST, JW GOETHE-UNIV, SIESMAYERSTR 70, 6000 FRANFKFURT/MAIN, FRG**WEST GERMANY
JOURNAL: Biochimica et Biophysica Acta 973 (2): p131-137 1989
ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Preillumination with light 1 strongly diminishes the apparent quantum yield of Photosystem I in Porphyridium purpureum, %%%Porphyra%%% yezoensis and some other red algae. At limiting light 1 intensities, the photooxidation rate of %%%cytochrome%%% f and of P-700 is reduced by 40-60% after preillumination with light 1 compared with light 2 preillumination. Addition of DCMU or DBMIB preceding the preillumination period completely abolishes the effect, whilst addition immediately after the preillumination does not affect it. We concluded that this effect (1) is not realted to a redistribution of energy, (2) is not caused by an acceleration of the simultaneous reduction of %%%cytochrome%%% f and P-700 via plastoquinone (by cyclic or noncyclic electron transport) and (3) depends on the redox state of an electron carrier nearly connected with the plastoquinone pool. In many respects, as in fluorescence or oxygen-exchange kinetics, this effect mimics the phenomena which are expected to result from a true redistribution of excitation energy

between the two photosystems.

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DIALOG(R)File 5:Biosis Previews(R)

09256271 BIOSIS NO.: 198886096192
ALGAL HEME OXYGENASE FROM CYANIDIUM-CALDARIUM PARTIAL PURIFICATION AND FRACTIONATION INTO THREE REQUIRED PROTEIN COMPONENTS
AUTHOR: CORNEJO J (Reprint); BEALE S I
AUTHOR ADDRESS: DIV BIOL, MED, BROWN UNIV, PROVIDENCE, RI 02912, USA**USA
JOURNAL: Journal of Biological Chemistry 263 (24): p11915-11921 1988
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Enzymatic heme oxygenase activity has been partially purified from extracts of the unicellular red alga Cyanidium caldarium, and the macromolecular components have been separated into three protein fractions, referred to as Fractions I, II, and III, by serial column chromatography through DEAE-cellulose and Reactive Blue 2-Sepharose. Fraction I is retained by DEAE-cellulose at low salt concentration and eluted by 1 M NaCl. Fraction II is retained by Blue Sepharose at low salt concentration and eluted by 1 M NaCl. Fraction III is retained on 2', 5'-ADP-agarose and eluted by 1 mM NADPH, while Fraction II is not retained on ADP-agarose. Fractions I-III, have Mr values of 22,000, 38,000, and 37,000, respectively (all .+-. 2,000), as determined by Sephadex gel filtration chromatography. In vitro heme oxygenase activity requires the presence of all three fractions, plus substrate, O2, reduced pyridine nucleotide, and another reductant. Ascorbate, isoascorbate, and phenylenediamine serve equally well as the second reductant, but hydroquinone can also be used, with lower activity resulting. Fractions I-III are heat sensitive and inactive by Pronase digestion. Fraction I has a visible absorption spectrum similar to that of ferredoxin and is bleached by dithionite reduction or incubation with p-hydroxymercuribenzoate. Fraction I can be replaced by commercially available ferredoxin derived from the red alga %%%Porphyra%%% umbilicalis, and to a smaller extent, by spinach ferredoxin. Fraction III contains ferredoxin-linked cytoxhrome c reductase activity and can be partially replaced by spinach ferredoxin-NADP+ oxidoreductase. Reconstituted heme oxygenase and ferredoxin-linked %%%cytochrome%%% c reductase activities are both abolished if Fraction I or III is preincubated with 0.1 mM p-hydroxymercuribenzoate, but heme oxygenase activity is only slightly affected if Fraction II is preincubated with p-hydroxymercuribenzoate. Preincubation of Fraction II with 0.5 mM diethylpyrocarbonate inactivates heme oxygenase in the reconstituted system, and 10 .mu.M mesohemin partially protects this Fraction against diethylpyrocarbonate inactivation. Algal heme oxygenase is inhibited 80% by 2 .mu.M Sn-protoporphyrin even in the presence of 20 .mu.M mesohemin. Fraction II is rate limiting in unfractionated and reconstituted incubation mixtures. None of the three cell fractions could be replaced by bovine spleen microsomal heme oxygenase or NADPH-%%%cytochrome%%% P450 reductase.

1/7/17
DIALOG(R)File 5:Biosis Previews(R)

06567804 BIOSIS NO.: 198273071731
STUDIES ON ALGAL CYTOCHROMES 3. AMINO-ACID SEQUENCE OF %%%CYTOCHROME%%% C-553 FROM A BROWN ALGA PETALONIA-FASCIA
AUTHOR: SUGIMURA Y (Reprint); HASE T; MATSUBARA H; SHIMOKORIYAMA M
AUTHOR ADDRESS: DEP BIOL, FACULTY SCI, TOHO UNIV, FUNABASHI, CHIBA 274** JAPAN
JOURNAL: Journal of Biochemistry (Tokyo) 90 (4): p1213-1220 1981
ISSN: 0021-924X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The amino acid sequence of a photosynthetic %%%cytochrome%%% c-553 isolated from a brown alga, P. fascia was determined by BrCN fragmentation and a solid phase Edman degradation. The %%%cytochrome%%% contains 85 amino acid residues, giving a MW of 9803. The complete amino acid sequence is given. The highest homology occurred between the sequences of cytochromes c-553 of P. fascia and Alaria esculenta, the next between those of P. fascia and %%%Porphyra%%% tenera.

1/7/18
DIALOG(R)File 5:Biosis Previews(R)

06008513 BIOSIS NO.: 198070040000
ELECTRON DONATION TO PHOTOSYSTEM I
AUTHOR: DAVIS D J (Reprint); KROGMANN D W; SAN PIETRO A
AUTHOR ADDRESS: DEP BIOL, INDIANA UNIV, BLOOMINGTON, INDIANA 47405, USA** USA
JOURNAL: Plant Physiology (Rockville) 65 (4): p697-702 1980
ISSN: 0032-0889
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Electron donation to photosystem I was studied in highly resolved particles from spinach. Divalent cations increased the efficiency of electron donation from spinach plastocyanin to P700+ through a decrease in the apparent Km for plastocyanin. %%%Cytochrome%%% f was not an efficient electron donor for P700+ in the presence or absence of divalent cations. %%%Cytochrome%%% f photooxidation could be observed in the presence of both plastocyanin and divalent cations. The efficiencies of electron donors from eukaryotic and prokaryotic algae [Porphyridium cruentum, %%%Porphyra%%% tenera, Microcystis aeruginosa, Anabaena variabilis, Aphanizomemon flosaquae, Agmenella quadruplecandata and Spirullina maxima] to P700+ were also examined. Divalent cations enhanced the effectiveness of electron donors from eukaryotic organisms while inhibiting electron donors from prokaryotic organisms. The prokaryotic electron donors were also much more efficient donors than were the electron donors from eukaryotic organisms. A correlation between the Km for the electron donor and its isoelectric point suggests that the net charge on the donor protein is a major determinant of the efficiency for

electron donation. The data presented raise interesting questions with respect to the evolution of electron donation to photosystem I and the possibility of an additional electron carrier between plastocyanin and P700+.

1/7/19
DIALOG(R)File 5:Biosis Previews(R)

05865790 BIOSIS NO.: 198019042279
SEQUENCE HOMOLOGY OF %%%CYTOCHROME%%% OXIDASE SUBUNITS TO ELECTRON CARRIERS OF PHOTO PHOSPHORYLATION
BOOK TITLE: SCHAEFER, G. AND M. KLINGENBERG (ED.). COLLOQUIUM DER GESELLSCHAFT FUER BIOLOGISCHE CHEMIE (COLLOQUIUM OF THE SOCIETY FOR BIOLOGICAL CHEMISTRY), VOL. 29. ENERGY CONSERVATION IN BIOLOGICAL MEMBRANES, APR. 6-8, 1978. XIV+287P. SPRINGER-VERLAG: NEW YORK, N.Y., USA; BERLIN, WEST GERMANY. ILLUS
AUTHOR: BUSE G (Reprint)
AUTHOR ADDRESS: ABT PHYSIOL CHEM, RHEINISCH-WESTFAEL TECH HOCHSCH AACHEN, MELATENERSTR 211, 5100 AACHEN, W GER**WEST GERMANY
SERIES TITLE: Colloquium der Gesellschaft fuer Biologische Chemie in Mosbach pP53-55 1978
ISSN: 0366-5887 ISBN: 0-387-09079-7; 3-540-08560-2
DOCUMENT TYPE: Book Chapter; Meeting; Meeting Paper
RECORD TYPE: Citation
LANGUAGE: ENGLISH

1/7/20
DIALOG(R)File 5:Biosis Previews(R)

05126447 BIOSIS NO.: 197763047303
ROLE OF CYCLIC ELECTRON TRANSPORT IN PHOTOSYNTHESIS AS MEASURED BY THE PHOTO INDUCED TURNOVER OF P-700 IN-VIVO
AUTHOR: MAXWELL P C; BIGGINS J
JOURNAL: Biochemistry 15 (18): p3975-3981 1976
ISSN: 0006-2960
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: The light-induced turnover of P700 was measured spectrophotometrically in a wide variety of algae [Porphyridium cruentum, Chlorella pyrenoidosa, Anacystis nidulans, Scenedesmus obliquus, Aphanocapsa, Skeletonema costatum, Cryptochrysis sp., Euglena gracilis, Ulva lactuca, %%%Porphyra%%% umbilicalis, Chlamydomonas reinhardi] and some photosynthetic mutants. Analysis of the postillumination recovery of P700+ revealed that the apparent 1st-order rate constant for reduction via the cyclic pathway was much lower than that via the noncyclic pathway. After activation of photosystems 1 and 2 the half-time [t 1/2] for reduction of P700+ was 5-20 ms, whereas after activation of primarily photosystem 1 a longer t 1/2 of approximately 150 ms was observed. The extent of the photooxidation of P700 was the same in both regimes of illumination. The longer t 1/2 was also noted after inhibition of photosystem 2 by 3-(3,4-dichlorophenyl)-1,1-dimethylurea or mild heat

shock and in mutant algae known to lack a functional photosystem 2. No signal was observed in mutants lacking P700 itself but those strains lacking either plastocyanin or %%%cytochrome%%% f were capable of a very slow turnover (reduction t 1/2 > 500 ms at room temperature). This very slow turnover was not affected by carbonyl cyanide m-chlorophenylhydrazone or the plastoquinone antagonist, 2,5-dibromo-3-methyl-6-isopropyl-p-benzoquinone, indicating that the pathway for reduction of P700+ in these mutants is not energy linked and does not utilize the intersystem electron transport chain. The slow, 150 ms, reduction of P700+ due to cyclic flow was not observed when cells were engaged in photosynthesis at high-light intensities. The data are interpreted as evidence for the involvement of the total functional pool of P700 in both electron transport pathways, and cyclic electron transport probably does not contribute to photosynthesis in O2-evolving autotrophs.

1/7/21
DIALOG(R)File 5:Biosis Previews(R)

05083660 BIOSIS NO.: 197763004516
NITRITE REDUCING ACTIVITY OF MODIFIED %%%CYTOCHROME%%% C-553 FROM THE RED ALGA %%%PORPHYRA%%%-YEZOENSIS
AUTHOR: HO C-H; IKAWA T; NISIZAWA K
JOURNAL: Plant and Cell Physiology 17 (3): p431-438 1976
ISSN: 0032-0781
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: Crystalline %%%cytochrome%%% c-553 was obtained from P. yezoensis Ueda. The %%%cytochrome%%% in a reduced form was modified to show a nitrite-reducing activity after appropriate treatment with heat, hydrogen peroxide, or photooxidation using methylene blue as the electron acceptor, but the reducing activity was far lower than that of the nitrite reductase isolated from this alga. The modified %%%cytochrome%%% c-553 was autooxidizable and showed an absorption spectrum resembling that of %%%cytochrome%%% c-553 in the oxidized form except for slight shifts of the absorption maximum in the .gamma.-band region toward shorter wavelengths.

1/7/22
DIALOG(R)File 5:Biosis Previews(R)

04920413 BIOSIS NO.: 197662016552
EFFECTS OF SOME CULTURAL CONDITIONS UPON THE NITRITE REDUCTASE ACTIVITY IN %%%PORPHYRA%%%-YEZOENSIS
AUTHOR: HO C-H; ARAKI S; IKAWA T; NISIZAWA K
JOURNAL: Bulletin of the Japanese Society of Phycology 23 (3): p87-92 1975
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

1/7/23
DIALOG(R)File 5:Biosis Previews(R)

04850497 BIOSIS NO.: 197661016636
%%%CYTOCHROME%%% C-S FROM RHODYMENIA-PALMATA AND %%%PORPHYRA%%%-UMBILICALIS AND THE AMINO-ACID SEQUENCES OF THEIR N TERMINAL REGIONS
AUTHOR: MEATYARD B T; SCAWEN M D; RAMSHAW J A M; BOULTER D
JOURNAL: Phytochemistry (Oxford) 14 (7): p1493-1497 1975
ISSN: 0031-9422
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

1/7/24
DIALOG(R)File 5:Biosis Previews(R)

04715309 BIOSIS NO.: 197560051448
THE AMINO-ACID SEQUENCE OF %%%CYTOCHROME%%% F FROM THE BROWN ALGA ALARIA-ESCULENTA
AUTHOR: LAYCOCK M V
JOURNAL: Biochemical Journal 149 (1): p271-280 1975
ISSN: 0264-6021
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

1/7/25
DIALOG(R)File 5:Biosis Previews(R)

04501872 BIOSIS NO.: 197511008015
THE PHOTOCHEMICAL REACTIONS OF PHOTOSYNTHESIS IN AN ALGA EXPOSED TO EXTREME CONDITIONS
BOOK TITLE: CARNEGIE INST WASH. CARNEGIE INSTITUTION OF WASHINGTON YEAR BOOK 1972. VII+777P. ILLUS. CARNEGIE INSTITUTION: WASHINGTON, D.C., U.S.A
AUTHOR: FORK D C; HIYAMA T
p384-388 1973
DOCUMENT TYPE: Book
RECORD TYPE: Citation
LANGUAGE: Unspecified

1/7/26
DIALOG(R)File 5:Biosis Previews(R)

03714185 BIOSIS NO.: 197152080711
OXIDATION REDUCTION REACTIONS OF PHYTOCHROME 700 AND %%%CYTOCHROME%%% F IN FRACTION 1 PARTICLES PREPARED FROM SPINACH-D CHLOROPLASTS BY FRENCH PRESS TREATMENT
AUTHOR: FORK D C; MURATA N
JOURNAL: Photochemistry and Photobiology 13 (1): p33-44 1971
ISSN: 0031-8655

DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

1/7/27
DIALOG(R)File 5:Biosis Previews(R)

03231505 BIOSIS NO.: 196950049657
%%%CYTOCHROME%%% REACTIONS IN PORPHYRIDIUM AND %%%PORPHYRA%%% REACTION TIMES AND STRUCTURAL RIGIDITY
BOOK TITLE: %%%CYTOCHROME%%% REACTIONS IN PORPHYRIDIUM AND %%%PORPHYRA%%% REACTION TIMES AND STRUCTURAL RIGIDITY
AUTHOR: NISHIMURA M
p196-200 1968
DOCUMENT TYPE: Book
RECORD TYPE: Citation
LANGUAGE: Unspecified

1/7/28
DIALOG(R)File 5:Biosis Previews(R)

0001905443 BIOSIS NO.: 19684900064085
Comparative studies of photochemical oxidation-reduction reactions in lamellar fragments of various algae and spinach
AUTHOR: MURANO FUMIO; FUJITA YOSHIHIKO
AUTHOR ADDRESS: Ocean Res. Inst., Univ., Tokyo, Jap.,
JOURNAL: PLANT CELL PHYSIOL 8 ((4)): p673-682 1967 1967
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: The activity of various electron carriers, including DPIP [2,6-dichloro-phenolindophenol], spinach plastocyanin, mammalian %%%cytochrome%%% c, and Anabaena %%%cytochrome%%% 553, as donor in the reaction induced by the photochemical system I was examined with lamellar fragments of various algae and spinach. Reduced DPIP was an effective electron donor irrespective of the organisms, when it was supplied at a high concentration (10-3 m). Spinach plastocyanin was effective in the reactions with the lamellae of green algae, Euglena, diatom Phaeodacty-rum and red algae %%%Porphyra%%% yezoensis and %%%Porphyra%%% sp. Yamamoto n, whereas it was inactive in the lamellae of blue-green algae. Horse-heart %%%cytochrome%%% c and Anabaena %%%cytochrome%%% 553 were active in the reaction with the lamellae of blue-green algae. The former %%%cytochrome%%% was also active in the reactions in Porphyridium and Cyanidium. The cytochromes were less active in the reactions in which spinach plastocyanin acted as effective electron donor. The data were interpreted as that the photochemical system I in blue-green algae differs from that of other photosynthetic organisms with respect to the properties of the site of the electron-input. ABSTRACT AUTHORS: Authors

1/7/29
DIALOG(R)File 5:Biosis Previews(R)

0001905417 BIOSIS NO.: 19684900064059
Transfer of energy between reaction centers of photosystem 1 in algae
AUTHOR: FORK DAVID C; AMESZ JAN
JOURNAL: CARNEGIE INST WASH YEARB 66 p155-160 1966/ 1967 1966
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: The relative efficiency of O2, evolution was compared with the oxidation level of P700 and of %%%cytochrome%%% f as a function of light intensity in Cryptopleura violacea, Ulva lobata, Schizothrix calcicola and in %%%Porphyra%%% perforata. ABSTRACT AUTHORS: From auths

1/7/30
DIALOG(R)File 5:Biosis Previews(R)

0001905400 BIOSIS NO.: 19684900064042
Role of P700 and cyto-chrome f in the reaction center of photosystem
AUTHOR: AMESZ JAN; FORK DAVID C
JOURNAL: CARNEGIE INST WASHYEARB 66 p149-155 1966/ 1967 1966
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: Light-induced reactions of P700, the presumed primary reactions of photosystem 1 and %%%cytochrome%%% f was studied in the red algae Iridaea splendens, Schizy-menia pacifica, and %%%Porphyra%%% perforata. ABSTRACT AUTHORS: From auth

1/7/31
DIALOG(R)File 5:Biosis Previews(R)

0001856296 BIOSIS NO.: 19684900014936
Oxidation-reduction reactions of cytochromes in red algae
AUTHOR: NISHIMURA MITSUO
AUTHOR ADDRESS: Univ. Pa., Johnson Res. Found., Philadelphia, Pa., USA
JOURNAL: BROOKHAVEN SYMP BIOL 19 p132-142 1966 1966
CONFERENCE/MEETING: Brookhaven National Laboratory: Energy conversion by the photosynthetic apparatus, Upton, N. Y., 6-9 June, 1966
DOCUMENT TYPE: Meeting
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: The light-induced and dark oxidation-reduction reactions of cyto-chrorae-553 and a b-type %%%cytochrome%%% in the living thalli, intact cells, and isolated particles of four species of red algae (%%%Porphyra%%% yezoensis, P. tenera, P. suborbiculata, and Porphyridium cruentum) were studied. The action spectrum of %%%cytochrome%%% oxidation had a maximum at 685 to 690 m[mu]. In the presence of background illumination of 680 to 700 m[mu], photochemical reduction by a 2nd light of wavelength shorter than 650 m[mu] was observed. The maxima of the

action spectrum for the reduction were located at 565 and at 615 to 620 m[mu]. This reduction of cytochromes by light absorbed by phycobilins was inhibited by bromoisopropylmethyluracil, chlorophenyldimethylurea, Simazine, dichloropropionanilide and o-phenanthroline. Carbonyl cyanide phenylhydrazone derivatives inhibited the reduction of a b-type %%%cytochrome%%% in the dark. Phenyl-mercuric acetate induced inhibition of dark reduction and light-induced reduction (by photochemical system II) of cytochromes. Values of quantum yield of photochemical reaction under different conditions were presented. Excitation of Porphyridium by a Q-switched laser flash revealed that the %%%cytochrome%%%- 553 oxidation took place within 40 usec with a half-rise time of 14 usec. A scheme is proposed for the photochemical and dark oxidation-reduction reactions in %%%Porphyra%%% and Porphyridium. ABSTRACT AUTHORS: Author

1/7/32
DIALOG(R)File 5:Biosis Previews(R)

0001824818 BIOSIS NO.: 19674800108485
Quenching of chlorophyll fluorescence by quinones in algae and chloroplasts
AUTHOR: AMESZ JAN; FORK DAVID C
AUTHOR ADDRESS: Biophys. Lab., Univ., Leiden, Neth.
JOURNAL: BIOCHIM BIOPHYS ACTA 143 ((1)): p97-107 1967 1967
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: A number of quinones and substituted quinones quenched strongly chlorophyll fluorescence in Swiss chard chloroplasts and in the intact algae, Ulva lobata and %%%Porphyra%%% perforata. Quenching occurred in the absence as well as in the presence of 3(3,4-dichlorophenyl)-1,1-dimethylurea. Among the quinones found to have a high quenching activity were 2,3,5,6-tetramethylbenzoquinone, 2-methyl-1, 4-naphthoquinone, 5-hydroxy-1,4-naphthoquinone, phenanthrenequinone, and 1,2-dihydroxyanthraquinone. Reduced quinones had no or little quenching activity. The quinones tested quenched less strongly the initialfluorescence, observed immediately upon illumination, than the subsequent rise of fluorescence yield during illumination. For the most active compounds, the concentrations needed for 50% quenching of the initial and the subsequent increase of fluorescence were about 70 and 15 [mu]M, respectively. The kinetics of fluorescence quenching at different light intensities and concentrations of quencher and absence of stimulation of O2 evolution indicate that the quenchers do not stimulate photosynthetic electron transport but interact directly with chlorophyll molecules of photosystem 2 by formation of traps for the excitation energy. In agreement with the assumption that the site of action of the quinones is near system 2, a number of these compounds inhibited light-induced %%%cytochrome%%% reduction in %%%Porphyra%%% in vivo. However, for most compounds no quantitative relation was found between the extent of inhibition of %%%cytochrome%%% reduction or of the Hill reaction in chloroplasts and the activity in quenching chlorophyll fluorescence. ABSTRACT AUTHORS: Authors

1/7/33
DIALOG(R)File 5:Biosis Previews(R)

0001792828 BIOSIS NO.: 19674800076833
Mechanism of two photochemical reactions in algae as studied by means of fluorescence
BOOK TITLE: Studies on microalgae and photosynthetic bacteria
AUTHOR: DUYSENS L N M; SWEERS H E
AUTHOR ADDRESS: Univ. Leiden, Nieuwsteeg 18, Leiden, Neth.
p353-372 1963
BOOK PUBLISHER: The University of Tokyo Press, Tokyo, Jap.
DOCUMENT TYPE: Book
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: By means of a new type of apparatus time curves of the fluorescence yield of photo-synthetic pigments were studied at various wavelengths of emission and excitation for Porphyridium cruentum, Chlorella, spinach, and spinach chloroplasts and a number of other species. The changes in fluorescence yield could be brought about by 2 actinic beams which did not directly cause a deflection of the recording apparatus. The apparatus was only sensitive to the modulated excitation beam. In all species studied the fluorescence yield of the chlorophyll [alpha]2 be- longing to the photochemical pigment system 2 (which is responsible for oxygen evolution and %%%cytochrome%%% reduction), decreased upon illumination with actinic light mainly absorbed by the pigment system 1 (which causes %%%cytochrome%%% oxidation and pyridine nucleotide reduction) and increased upon illumination with light mainly absorbed by system 2. These and other experiments indicate that the decrease is caused by the oxidation of a reactive molecule or "reaction center" The excitation energy is transferred from the chlorophyll [alpha]2 mole-cules to these reaction centers and is trapped if the center is in an oxidized state which is designated by Q. Upon excitation of system 2 the reaction center becomes reduced and an unknown precursor of oxygen becomes oxidized. The reduced reaction center, QH, does not trap the excitation energy and thus does not quench the fluorescence of chlorophyll [alpha]2, but is oxidized by a reaction excited by system 1. The inhibitor DCMU [3-(3[image], 4[image]-dichlorophenyl-1, 1 dimethylurea] prevents the reoxidation of QH. If the algae or spinach leaves are illuminated during more than a few seconds with light mainly absorbed by system 2, the initial rapid increase in chlorophyll [alpha]2 fluorescence is followed by a decrease. This decrease is attributed partly to an increase in the rate of the reoxidation of QH by system 1 and partly to a dark side reaction of QH which converts QH into a compound Q', which quenches the fluorescence and which is slowly converted into Q by a dark reaction. The conversion of QH into Q' is also inhibited by DCMU. Porphyridium cruentum and %%%Porphyra%%% sp. an increase in the steady state yield of fluorescence occurred not only in the chlorophyll a maximum, but also in rather broad bands at about 720 and 730 m[mu] respectively, upon switching from blue actinic light to green. In these algae blue light is mainly absorbed by system 1 and green light by system 2. The changes in fluorescence yield in the infrared bands were most pronounced for blue excitation which suggests that these bands are excited by pigment system 1. It is possible that the infrared fluorescing substance is the energy trap for system 1. No changes were observed in phycopilin fluorescence. ABSTRACT AUTHORS: Authors

1/7/34
DIALOG(R)File 5:Biosis Previews(R)

0001792619 BIOSIS NO.: 19674800076624
The role of C-type %%%cytochrome%%% in the Hill reaction with Euglena chloroplasts
AUTHOR: KATOH SAKAE; PIETRO ANTHONY SAN
AUTHOR ADDRESS: Charles F. Kettering Res. Lab., Yellow Springs, Ohio, USA
JOURNAL: ARCH BIOCHEM BIOPHYS 118 ((2)): p488-496 1967 1967
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: Euglena chloroplasts catalyze the Hill reaction with ferricyanide or dichloro-phenol indophenol (DPIP) but not with nicotinamide adenine dinucleo-tide phosphate (NADP), methyl viologen or horse-heart %%%cytochrome%%% c. The latter compounds can serve as Hill oxidants with Euglena chloro-plasts provided Euglena %%%cytochrome%%%-552 is included in the reaction mixture. This c-type %%%cytochrome%%% is solubilized during preparation of the algal chloroplasts. It acts in a catalytic fashion and appears to function in the electron transport chain which interconnects the two photosystems of photosynthesis. Euglena %%%cytochrome%%%-552 is most effective in restoration of NADP photoreduction activity; some restoration is observed with another algal c-type %%%cytochrome%%%, %%%Porphyra%%% tenera %%%cytochrome%%%-553. In contrast, restoration was not observed with either Euglena %%%cytochrome%%%-556 or horse-heart %%%cytochrome%%% c. ABSTRACT AUTHORS: Authors

1/7/35
DIALOG(R)File 5:Biosis Previews(R)

0001787404 BIOSIS NO.: 19674800071409
Photosynthetic electron transport chain of Chlamydomonas reinhardi. V. Purification and properties of %%%cytochrome%%% 553 and ferredoxin
AUTHOR: GORMAN DONALD S; LEVINE R P
AUTHOR ADDRESS: Charles F. Kettering Res. Lab., Yellow Springs, Ohio, USA
JOURNAL: PLANT PHYSIOL 41 ((10)): p1643-1647 1966 1966
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: %%%Cytochrome%%% 553 and ferredoxin were isolated and purified from acetone powders prepared from intact cells of the wild-type strain of C. reinhardi. Purification was achieved by ion exchange chromatography of DEAE cellulose and gel filtration on Sephadex G-75. %%%Cytochrome%%% 553 could be oxidized with potassium ferricyanide and reduced with sodium ascorbate. The apsorption maxima of the %%%cytochrome%%% in reduced form were found to be [alpha]-band 552.5 nm, [beta]-band 522.5 nm, and Soret band 416.5nm. The normal redox potential was +0.37 volt, and the molecular weight was estimated to be 12,000 [plus or minus] 2,000. The %%%cytochrome%%% closely resembled that of the c-type cytochromes extracted from Euglena and %%%Porphyra%%%. When cultures were harvested after they had entered stationary phase, the %%%cytochrome%%% could be

extracted in soluble form, and in some cases a yield of 1 %%%cytochrome%%%/1000 chlorophyll molecules could be obtained. Ferredoxin showed absorption maxima at 278, 330, 420, and 460 nm. Thus it resembles the ferredoxin extracted from spinach. The molecular weight of the ferredoxin was estimated to be 15,000[plus or minus] 2,000. ABSTRACT AUTHORS: Authors

1/7/36
DIALOG(R)File 5:Biosis Previews(R)

0001689681 BIOSIS NO.: 19664700093783
Energy- and electron-transfer systems in algal photosynthesis. I. Actions of two photochemical systems in oxidation-reduction reactions of %%%cytochrome%%% in %%%Porphyra%%%
AUTHOR: NISHIMURA MITSUO; TAKAMIYA ATUSI
AUTHOR ADDRESS: Johnson Res. Found., Univ. Penn., Philadelphia, Penn., USA
JOURNAL: BIOCHIM BIOPHYS ACTA 120 ((1)): p45-56 1966 1966
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: The light-induced oxidation-reduction reactions of %%%Porphyra%%% %%%cytochrome%%%-553 in the living thalli and isolated particles of three species of %%%Porphyra%%% (P. yezoensis, P. tenera and P. suborbiculata) were studied. The action spectrum of %%%cytochrome%%% oxidation had a maximum at 685-690 m.[mu] In the presence of background illumination of 680-700 m[mu], photochemical reduction by a second light of wavelengths shorter than 650 m[mu]. was observed. The maxima of the action spectrum for the reduction were located at 565 m[mu] and 615-620 m[mu]. This reduction of %%%cytochrome%%% by light absorbed by phycobilins was inhibited by 5-bromo-3- isopropyl-6-methyluracil, 3(4[image]-chlorophenyl)-1, 1-dimethylurea, 2-chloro-4, 6-bis-(ethylamino)-1, 3, 5-triazine, 3, 4-dichloropropionanilide and o-phenanthroline. These substances neither inhibited the light-induced oxidation of %%%cytochrome%%%, nor the dark reduction of %%%cytochrome%%% . In the presence of these substances, light-induced oxidation of %%%cytochrome%%% was observed on illumination of the light absorbed by phycobilins as well as by chlorophyll a. Effects of incident light intensity, dark period, inhibitors, gas phase, etc. on the rates and the steady-state change of the %%%cytochrome%%% reactions were investigated. Comparison of the observed amounts of %%%cytochrome%%% change and the amounts of %%%cytochrome%%%-553 extracted from the thalli indicated that the major portion of the %%%cytochrome%%%-553 present in the thalli changed its oxidation-reduction state on illumination. The quantum yield of %%%cytochrome%%% oxidation by light absorbed by chlorophyll a was about 0. 14. In the presence of 5-bromo-3-isopropyl-6-methyluracil, quantum yields with light absorbed by chlorophyll a and with light absorbed by phycobilins were about 0. 15 and 0. 11, respectively. ABSTRACT AUTHORS: Authors

1/7/37
DIALOG(R)File 5:Biosis Previews(R)

0001581219 BIOSIS NO.: 19654600095434
Light-induced changes in absorbancy and fluorescence of chlorophyllous pigments associated with the pigment systems 1 and 2 in blue-green algae
AUTHOR: VREDENBERG W J; DUYSENS L N M
AUTHOR ADDRESS: Biophys. Lab., State Univ., Leiden, Neth.
JOURNAL: BIOCHIM BIOPHYS ACTA 94 ((2)): p355-370 1965 1965
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: The kinetics and the difference spectra of light-induced changes in absorbancy and of changes in the near infrared fluorescence were measured in the blue-green algae Schizothrix calcicola and Anacystis nidulans. The action spectrum of the photooxidation of P 700 in Schizothrix was measured in the presence of 3-(3,4-dichloro-phenyl)-I,I-dimethylurea at 2[degree]. The following quantum requirements q(A), for actinic wavelength [lambda] were estimated for P 700 and %%%cytochrome%%% oxidation and for P 700 reduction. Schizothrix P 700 oxidation, q(680m[mu]) varies between 2.0 and 2.6, and q(430 m[mu]) between 5.6 and 6.4; %%%cytochrome%%% oxidation, q(680 m[mu]) =3.0-3.5; P 700 reduction, q(680 m/x) = 3.0. Anacystis: %%%cytochrome%%% oxidation, q(680 mji) = 2.8. The requirements per quantum absorbed by the photochemical system responsible for the reaction will be lower. The results are not inconsistent with the assumption that the true quantum requirement for the photochemical transport of I electron is 1 for each of the two pigment systems. A new "differential" flow attachment for a fluorescence apparatus was constructed by means of which small changes in fluorescence could be measured with increased precision, because the noise due to actinic light was eliminated. In addition to the earlier observed light-induced changes in the fluorescence of chlorophyll a2, a relatively small light-induced increase in red fluorescence, excited by blue light, was observed in Schizothrix calcicola, Porphyridium cruentum, and %%%Porphyra%%% sp. It was activated by Pigment System 1, was not reversed by light of System 2, and was not associated with redox changes of P 700. The difference spectrum of this fluorescence was different from that of chlorophyll [alpha]2-in having a higher hump at 720 m[mu].. ABSTRACT AUTHORS: Authors

1/7/38
DIALOG(R)File 5:Biosis Previews(R)

0001535055 BIOSIS NO.: 19654600049151
Mechanism of two photochemical reactions in algae as studied by means of fluorescence
BOOK TITLE: Japanese Society of Plant Physiologists, Editors. Studies on Microalgae and Photosynthesis Bacteria
AUTHOR: DUYSENS L N M; SWEERS H E
AUTHOR ADDRESS: Biophys. Lab. Univ. Leiden, Leiden, Netherlands
p353-372 1963
BOOK PUBLISHER: Japanese Society of Plant Physiology, University of Tokyo Press, Tokyo, Japan
DOCUMENT TYPE: Book
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: By means of a new type of apparatus, time curves of the fluorescence yield of photosynthetic pigments were studied at various wavelengths of emission and excitation for the red alga Porphyridium cruentum, the green alga Chlorella, spinach and spinach chloroplasts, and a number of other sp. The changes in fluorescence yield could be brought about by 2 actinic beams which did not directly cause a deflection of the recording apparatus. The apparatus was only sensitive to the modulated excitation beam. In all sp. studied, the fluorescence yield of chlorophyll a2 belonging to the photochemical pigment system 2 (which is responsible for oxygen evolution and %%%cytochrome%%% reduction), decreased upon illumination with actinic light mainly absorbed by the pigment system 1 (which causes %%%cytochrome%%% oxidation and pyridine nucleotide reduction) and increased upon illumination with light mainly absorbed by system 2. These and other experiments indicate that the decrease is caused by the oxidation of a reactive molecular or "reaction center." The excitation energy is transferred from the chlorophyll a2 molecules to these reaction centers and is trapped if the center is in an oxidized state which is designated by Q. Upon excitation of system 2 the reaction center becomes reduced and an unknown precursor of oxygen becomes oxidized. The reduced reaction center, QH, does not trap the excitation energy and thus does not quench the fluorescence of chlorophyll i.% but is oxidized by a reaction excited by system 1. The inhibitor DCMU prevents the reoxidation of QH. If the algae or spinach leaves are illuminated during more than a few seconds with light mainly absorbed by system 2, the initial rapid increase in chlorophyll a2 fluorescence is followed by a decrease. This decrease is attributed partly to an increase in the rate of the reoxidation of QH by system 1 and partly to a dark side reaction of QH which converts QH into a compound Q[image] which quenches the fluorescence and which is slowly converted into Q by a dark reaction. The conversion of QH into Q[image] is also inhibited by DCMU. In P. cruentum and %%%Porphyra%%% sp. an increase in the steady state yield of fluorescence occurred not only in the chlorophyll a maximum, but also in rather broad bands at about 720 and 730 m[mu]. respectively, upon switching from blue actinic light to green. In these algae blue light is mainly absorbed by system 1 and green light by system 2. The changes in fluorescence yield in the infrared bands were most pronounced for the excitation which suggests that these bands are excited by pigment system 1. It is possible that the infra-red fluorescing substance is the energy trap for system 1. No changes were observed in phycobilin fluorescence. ABSTRACT AUTHORS: Authors

1/7/39
DIALOG(R)File 5:Biosis Previews(R)

0001209431 BIOSIS NO.: 19623800007103
Studies on the mechanism of nitrogen assimilation in marine algae VIII. On the electron carrier of nitrate reductase in %%%Porphyra%%% yezoensis
AUTHOR: TAKAGI; MITSUZO; MURATA KIICHI
JOURNAL: BULL FAC FISH HOKKAIDO UNIV 6 ((1)): p33-36 1955 1955
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: Experiments were made to ascertain whether methylene blue, coenzyme 1(DPN) and %%%cytochrome%%% C are able or unable to fulfill a

specific function as an electron carrier of nitrate reductase in %%%Porphyra%%% yezoensis. The results obtained are summarized as follows Methylene blue can stand as a representative of an electron carrier of nitrate reductase. %%%Cytochrome%%% C is one of the real electron carriers of nitrate reductase. Coenzyme 1(DPN) is not separately able to act as an electron carrier of nitrate reductase. ABSTRACT AUTHORS: Authors

1/7/40
DIALOG(R)File 5:Biosis Previews(R)

0001140144 BIOSIS NO.: 19613600050054
Studies on algal %%%cytochrome%%%. II. Physico-chemical properties of crystalline %%%Porphyra%%% tenera %%%cytochrome%%% 553
AUTHOR: KATOH SAKAE
AUTHOR ADDRESS: U. Tokoy, Japan
JOURNAL: PLANT AND CELL PHYSIOL 1 ((2)): p91-98 1960 1960
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: The physico-chemical properties of an algal %%%cytochrome%%%, P. tenera %%%cytochrome%%% 553 were investigated, using a crystalline preparation of the substance. The %%%cytochrome%%% was found to be highly resistant to heat and preservation. The stability of the %%%cytochrome%%% was also prominent in a wide range of pH. Absorption spectra as well as data concerning the extinction coefficients of the oxidized and reduced forms are presented. The oxidation-reduction potential of the %%%cytochrome%%% was determined at various pH. The value for the normal potential was found to decrease gradually with increasing pH, from 355mV at pH 5.0, to 270mV at pH 11.0. Electrophoretic investigation revealed that this %%%cytochrome%%% is a markedly acidic protein, with an isolectric point of pH 3.5. The molecular weight of the %%%cytochrome%%% was determined from ultracentrifugal and diffusion experiments to be 13,600. The values for the minimum molecular weight calculated from the heme- and iron-contents are, respectively, 12,000 and 11,000. ABSTRACT AUTHORS: Author

1/7/41
DIALOG(R)File 5:Biosis Previews(R)

0001140141 BIOSIS NO.: 19613600050051
Some properties of %%%cytochrome%%% C from %%%Porphyra%%% tenera
AUTHOR: HASHIMOTO K; MASUHIRO I
JOURNAL: BULL JAPANESE SOC SCI FISH 25 ((7/9)): p561-564 1959 1959
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: %%%Cytochrome%%% c (Cyt) was purified from the alga. The preparation, containing 0.474% iron, proved to be electrophoretically homogeneous at various pH> s. The visible absorption spectra of the Cyt showed distinguishing characteristics, especially in the reduced form in

0.1 [image] acetate buffer of pH 6.0, the extinction coefficient of [alpha] maximum (at 553 m[mu]) was only about 3/4 of that of vertebrate %%%cytochrome%%%. In addition the whole spectrum shifted towards longer wave lengths than that of vertebrate Cyt; in 0.2 [image] NaOH, the whole spectrum was similar to that of vertebrates, both in positions and in extinction coefficients of maxima or minimum, and the extinction coefficient of a maximum was higher than that in the acetate buffer. Such a large difference of spectrum caused by change in pH has not been reported for %%%cytochrome%%% from any source. The pH-mobility curve of this protein also differed considerably from that of the horse. The isoelectric point was found to be around pH 4, which forms a marked contrast to vertebrate %%%cytochrome%%% (above pH 10). ABSTRACT AUTHORS: G. Gunter

1/7/42
DIALOG(R)File 5:Biosis Previews(R)

0001140087 BIOSIS NO.: 19613600049997
Studies on algal %%%cytochrome%%%. I. Enzymic activities pertaining to %%%Porphyra%%% tenera %%%cytochrome%%% 553 in cell-free extracts
AUTHOR: KATOH SAKAE
AUTHOR ADDRESS: U. Tokyo, Japan
JOURNAL: PLANT AND CELL PHYSIOL 1 ((1)): p29-38 1959 1959
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ordered

cyt c

ABSTRACT: Enzymic activities pertaining to P. tenera cyto-chrome 553 were investigated with cell-free extracts of a red alga, P. tenera, and various fractions prepared therefrom. The algal extracts were found to be incapable, in the dark, of catalyzing oxidation of reduced %%%cytochrome%%% 553 at a rate sufficient to account for the respiratory oxygen-uptake in the intact cell. Oxidation of %%%cytochrome%%% 553 was highly accelerated on illumination. The former reaction was found to be cyanide-sensitive and the latter, cyanide-insensitive. Both activities were found to be localized in the particulate fraction of the cell extract. Significant activities of reduced pyridine nucleotide-%%%cytochrome%%% reductase were discovered in the soluble fraction of the cell extract, the reaction being 2 or 3 times faster with TPNH than with DPNH as electron donor. There was no reaction with succinate in the presence of %%%cytochrome%%% and 2,6-dichlorophenol indophenol. P. tenera %%%cytochrome%%% 553 was shown to be localized in the plastids of the algal cell. Possible functions of %%%cytochrome%%% 553 in the algal metabolism are discussed. ABSTRACT AUTHORS: Author

1/7/43
DIALOG(R)File 5:Biosis Previews(R)

0001060132 BIOSIS NO.: 19603500042571
Crystallization of an algal %%%cytochrome%%%, %%%Porphyra%%% tenera-%%%cytochrome%%% 553
AUTHOR: KATOH SAKAE
AUTHOR ADDRESS: U. of Tokyo, Japan

JOURNAL: NATURE 186 ((4719)): p138-139 1960 1960
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

ordered

1/7/44
DIALOG(R)File 5:Biosis Previews(R)

0001042539 BIOSIS NO.: 19603500024974
Preparation of crystalline %%%cytochrome%%% from %%%Porphyra%%% tenera
AUTHOR: YAKUSHIJI EIJIRO; SUGIMURA YASUTOMO; SEKUZU ICHIRO; MORIKAWA ICHIRO ; OKUNUKI KAZUO
AUTHOR ADDRESS: Toho U., Narashino, Chiba, Japan
JOURNAL: NATURE 185 ((4706)): p105-106 1960 1960
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

ordered

? t s4/7/1-4

4/7/1
DIALOG(R)File 5:Biosis Previews(R)

06567804 BIOSIS NO.: 198273071731
STUDIES ON ALGAL CYTOCHROMES 3. AMINO-ACID SEQUENCE OF %%%CYTOCHROME%%% %%%C%%%-553 FROM A BROWN ALGA PETALONIA-FASCIA
AUTHOR: SUGIMURA Y (Reprint); HASE T; MATSUBARA H; SHIMOKORIYAMA M
AUTHOR ADDRESS: DEP BIOL, FACULTY SCI, TOHO UNIV, FUNABASHI, CHIBA 274** JAPAN
JOURNAL: Journal of Biochemistry (Tokyo) 90 (4): p1213-1220 1981
ISSN: 0021-924X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ordered

ABSTRACT: The amino acid sequence of a photosynthetic %%%cytochrome%%% %%%c%%%-553 isolated from a brown alga, P. fascia was determined by BrCN fragmentation and a solid phase Edman degradation. The %%%cytochrome%%% contains 85 amino acid residues, giving a MW of 9803. The complete amino acid sequence is given. The highest homology occurred between the sequences of cytochromes c-553 of P. fascia and Alaria esculenta, the next between those of P. fascia and %%%Porphyra%%% %%%tenera%%%.

4/7/2
DIALOG(R)File 5:Biosis Previews(R)

05865790 BIOSIS NO.: 198019042279
SEQUENCE HOMOLOGY OF %%%CYTOCHROME%%% OXIDASE SUBUNITS TO ELECTRON CARRIERS OF PHOTO PHOSPHORYLATION
BOOK TITLE: SCHAEFER, G. AND M. KLINGENBERG (ED.). COLLOQUIUM DER GESELLSCHAFT FUER BIOLOGISCHE CHEMIE (COLLOQUIUM OF THE SOCIETY FOR

BIOLOGICAL CHEMISTRY), VOL. 29. ENERGY CONSERVATION IN BIOLOGICAL MEMBRANES, APR. 6-8, 1978. XIV+287P. SPRINGER-VERLAG: NEW YORK, N.Y., USA; BERLIN, WEST GERMANY. ILLUS
AUTHOR: BUSE G (Reprint)
AUTHOR ADDRESS: ABT PHYSIOL CHEM, RHEINISCH-WESTFAEL TECH HOCHSCH AACHEN, MELATENERSTR 211, 5100 AACHEN, W GER**WEST GERMANY
SERIES TITLE: Colloquium der Gesellschaft fuer Biologische Chemie in Mosbach pP53-55 1978
ISSN: 0366-5887 ISBN: 0-387-09079-7; 3-540-08560-2
DOCUMENT TYPE: Book Chapter; Meeting; Meeting Paper
RECORD TYPE: Citation
LANGUAGE: ENGLISH

4/7/3
DIALOG(R)File 5:Biosis Previews(R)

0001792619 BIOSIS NO.: 19674800076624
The role of C-type %%%cytochrome%%% in the Hill reaction with Euglena chloroplasts
AUTHOR: KATOH SAKAE; PIETRO ANTHONY SAN
AUTHOR ADDRESS: Charles F. Kettering Res. Lab., Yellow Springs, Ohio, USA
JOURNAL: ARCH BIOCHEM BIOPHYS 118 ((2)): p488-496 1967 1967
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: Euglena chloroplasts catalyze the Hill reaction with ferricyanide or dichloro-phenol indophenol (DPIP) but not with nicotinamide adenine dinucleo-tide phosphate (NADP), methyl viologen or horse-heart %%%cytochrome%%% %%%c%%%. The latter compounds can serve as Hill oxidants with Euglena chloro-plasts provided Euglena %%%cytochrome%%%-552 is included in the reaction mixture. This c-type %%%cytochrome%%% is solubilized during preparation of the algal chloroplasts. It acts in a catalytic fashion and appears to function in the electron transport chain which interconnects the two photosystems of photosynthesis. Euglena %%%cytochrome%%%-552 is most effective in restoration of NADP photoreduction activity; some restoration is observed with another algal c-type %%%cytochrome%%%, %%%Porphyra%%% %%%tenera%%% %%%cytochrome%%% -553. In contrast, restoration was not observed with either Euglena %%%cytochrome%%%-556 or horse-heart %%%cytochrome%%% %%%c%%%. ABSTRACT AUTHORS: Authors

4/7/4
DIALOG(R)File 5:Biosis Previews(R)

0001140141 BIOSIS NO.: 19613600050051
Some properties of %%%cytochrome%%% %%%C%%% from %%%Porphyra%%% %%%tenera%%%
AUTHOR: HASHIMOTO K; MASUHIRO I
JOURNAL: BULL JAPANESE SOC SCI FISH 25 ((7/9)): p561-564 1959 1959
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: %%%Cytochrome%%% %%%c%%% (Cyt) was purified from the alga. The preparation, containing 0.474% iron, proved to be electrophoretically homogeneous at various pH> s. The visible absorption spectra of the Cyt showed distinguishing characteristics, especially in the reduced form in 0.1 [image] acetate buffer of pH 6.0, the extinction coefficient of [alpha] maximum (at 553 m[mu]) was only about 3/4 of that of vertebrate %%%cytochrome%%%. In addition the whole spectrum shifted towards longer wave lengths than that of vertebrate Cyt; in 0.2 [image] NaOH, the whole spectrum was similar to that of vertebrates, both in positions and in extinction coefficients of maxima or minimum, and the extinction coefficient of a maximum was higher than that in the acetate buffer. Such a large difference of spectrum caused by change in pH has not been reported for %%%cytochrome%%% from any source. The pH-mobility curve of this protein also differed considerably from that of the horse. The isoelectric point was found to be around pH 4, which forms a marked contrast to vertebrate %%%cytochrome%%% (above pH 10). ABSTRACT AUTHORS: G. Gunter

? t s2/7/1-13

2/7/1
DIALOG(R)File 5:Biosis Previews(R)

14205432 BIOSIS NO.: 199799839492
Cloning and sequence of a complementary DNA for red alga %%%cytochrome%%% f as a NO scavenger
AUTHOR: Kadokura Kazunari (Reprint); Yamada Seiji (Reprint); Saito Hiroko (Reprint); Nishio Toshiyuki (Reprint); Fukazawa Chikafusa; Oku Tadatake (Reprint)
AUTHOR ADDRESS: Dep. Biological Chem., Coll. Bioresource Sci., Nihon Univ., Setagaya, Tokyo, 154, Japan**Japan
JOURNAL: Japanese Journal of Pharmacology 75 (SUPPL. 1): p113P 1997 1997
CONFERENCE/MEETING: 5th International Meeting on the Biology of Nitric Oxide Kyoto, Japan September 15-19, 1997; 19970915
ISSN: 0021-5198
DOCUMENT TYPE: Meeting; Meeting Abstract; Meeting Poster
RECORD TYPE: Citation
LANGUAGE: English

2/7/2
DIALOG(R)File 5:Biosis Previews(R)

06567804 BIOSIS NO.: 198273071731
STUDIES ON ALGAL CYTOCHROMES 3. AMINO-ACID SEQUENCE OF %%%CYTOCHROME%%% C-553 FROM A BROWN ALGA PETALONIA-FASCIA
AUTHOR: SUGIMURA Y (Reprint); HASE T; MATSUBARA H; SHIMOKORIYAMA M
AUTHOR ADDRESS: DEP BIOL, FACULTY SCI, TOHO UNIV, FUNABASHI, CHIBA 274** JAPAN
JOURNAL: Journal of Biochemistry (Tokyo) 90 (4): p1213-1220 1981
ISSN: 0021-924X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: The amino acid sequence of a photosynthetic %%%cytochrome%%% c-553 isolated from a brown alga, P. fascia was determined by BrCN fragmentation and a solid phase Edman degradation. The %%%cytochrome%%% contains 85 amino acid residues, giving a MW of 9803. The complete amino acid sequence is given. The highest homology occurred between the sequences of cytochromes c-553 of P. fascia and Alaria esculenta, the next between those of P. fascia and %%%Porphyra%%% %%%tenera%%%.

2/7/3
DIALOG(R)File 5:Biosis Previews(R)

06008513 BIOSIS NO.: 198070040000
ELECTRON DONATION TO PHOTOSYSTEM I
AUTHOR: DAVIS D J (Reprint); KROGMANN D W; SAN PIETRO A
AUTHOR ADDRESS: DEP BIOL, INDIANA UNIV, BLOOMINGTON, INDIANA 47405, USA** USA
JOURNAL: Plant Physiology (Rockville) 65 (4): p697-702 1980
ISSN: 0032-0889
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Electron donation to photosystem I was studied in highly resolved particles from spinach. Divalent cations increased the efficiency of electron donation from spinach plastocyanin to P700+ through a decrease in the apparent Km for plastocyanin. %%%Cytochrome%%% f was not an efficient electron donor for P700+ in the presence or absence of divalent cations. %%%Cytochrome%%% f photooxidation could be observed in the presence of both plastocyanin and divalent cations. The efficiencies of electron donors from eukaryotic and prokaryotic algae [Porphyridium cruentum, %%%Porphyra%%% %%%tenera%%%, Microcystis aeruginosa, Anabaena variabilis, Aphanizomemon flosaquae, Agmenella quadruplecandata and Spirullina maxima] to P700+ were also examined. Divalent cations enhanced the effectiveness of electron donors from eukaryotic organisms while inhibiting electron donors from prokaryotic organisms. The prokaryotic electron donors were also much more efficient donors than were the electron donors from eukaryotic organisms. A correlation between the Km for the electron donor and its isoelectric point suggests that the net charge on the donor protein is a major determinant of the efficiency for electron donation. The data presented raise interesting questions with respect to the evolution of electron donation to photosystem I and the possibility of an additional electron carrier between plastocyanin and P700+.

2/7/4
DIALOG(R)File 5:Biosis Previews(R)

05865790 BIOSIS NO.: 198019042279
SEQUENCE HOMOLOGY OF %%%CYTOCHROME%%% OXIDASE SUBUNITS TO ELECTRON CARRIERS OF PHOTO PHOSPHORYLATION
BOOK TITLE: SCHAEFER, G. AND M. KLINGENBERG (ED.). COLLOQUIUM DER

GESELLSCHAFT FUER BIOLOGISCHE CHEMIE (COLLOQUIUM OF THE SOCIETY FOR BIOLOGICAL CHEMISTRY), VOL. 29. ENERGY CONSERVATION IN BIOLOGICAL MEMBRANES, APR. 6-8, 1978. XIV+287P. SPRINGER-VERLAG: NEW YORK, N.Y., USA; BERLIN, WEST GERMANY. ILLUS
AUTHOR: BUSE G (Reprint)
AUTHOR ADDRESS: ABT PHYSIOL CHEM, RHEINISCH-WESTFAEL TECH HOCHSCH AACHEN, MELATENERSTR 211, 5100 AACHEN, W GER**WEST GERMANY
SERIES TITLE: Colloquium der Gesellschaft fuer Biologische Chemie in Mosbach pP53-55 1978
ISSN: 0366-5887 ISBN: 0-387-09079-7; 3-540-08560-2
DOCUMENT TYPE: Book Chapter; Meeting; Meeting Paper
RECORD TYPE: Citation
LANGUAGE: ENGLISH

2/7/5
DIALOG(R)File 5:Biosis Previews(R)

04715309 BIOSIS NO.: 197560051448
THE AMINO-ACID SEQUENCE OF %%%CYTOCHROME%%% F FROM THE BROWN ALGA ALARIA-ESCULENTA
AUTHOR: LAYCOCK M V
JOURNAL: Biochemical Journal 149 (1): p271-280 1975
ISSN: 0264-6021
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

2/7/6
DIALOG(R)File 5:Biosis Previews(R)

0001856296 BIOSIS NO.: 19684900014936
Oxidation-reduction reactions of cytochromes in red algae
AUTHOR: NISHIMURA MITSUO
AUTHOR ADDRESS: Univ. Pa., Johnson Res. Found., Philadelphia, Pa., USA
JOURNAL: BROOKHAVEN SYMP BIOL 19 p132-142 1966 1966
CONFERENCE/MEETING: Brookhaven National Laboratory: Energy conversion by the photosynthetic apparatus, Upton, N. Y., 6-9 June, 1966
DOCUMENT TYPE: Meeting
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: The light-induced and dark oxidation-reduction reactions of cyto-chrorae-553 and a b-type %%%cytochrome%%% in the living thalli, intact cells, and isolated particles of four species of red algae (%%%Porphyra%%% yezoensis, P. %%%tenera%%%, P. suborbiculata, and Porphyridium cruentum) were studied. The action spectrum of %%%cytochrome%%% oxidation had a maximum at 685 to 690 m[mu]. In the presence of background illumination of 680 to 700 m[mu], photochemical reduction by a 2nd light of wavelength shorter than 650 m[mu] was observed. The maxima of the action spectrum for the reduction were located at 565 and at 615 to 620 m[mu]. This reduction of cytochromes by light absorbed by phycobilins was inhibited by bromoisopropylmethyluracil, chlorophenyldimethylurea, Simazine,

dichloropropionanilide and o-phenanthroline. Carbonyl cyanide phenylhydrazone derivatives inhibited the reduction of a b-type %%%cytochrome%%% in the dark. Phenyl-mercuric acetate induced inhibition of dark reduction and light-induced reduction (by photochemical system II) of cytochromes. Values of quantum yield of photochemical reaction under different conditions were presented. Excitation of Porphyridium by a Q-switched laser flash revealed that the %%%cytochrome%%%- 553 oxidation took place within 40 usec with a half-rise time of 14 usec. A scheme is proposed for the photochemical and dark oxidation-reduction reactions in %%%Porphyra%%% and Porphyridium. ABSTRACT AUTHORS: Author

2/7/7
DIALOG(R)File 5:Biosis Previews(R)

0001792619 BIOSIS NO.: 19674800076624
The role of C-type %%%cytochrome%%% in the Hill reaction with Euglena chloroplasts
AUTHOR: KATOH SAKAE; PIETRO ANTHONY SAN
AUTHOR ADDRESS: Charles F. Kettering Res. Lab., Yellow Springs, Ohio, USA
JOURNAL: ARCH BIOCHEM BIOPHYS 118 ((2)): p488-496 1967 1967
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: Euglena chloroplasts catalyze the Hill reaction with ferricyanide or dichloro-phenol indophenol (DPIP) but not with nicotinamide adenine dinucleo-tide phosphate (NADP), methyl viologen or horse-heart %%%cytochrome%%% c. The latter compounds can serve as Hill oxidants with Euglena chloro-plasts provided Euglena %%%cytochrome%%%-552 is included in the reaction mixture. This c-type %%%cytochrome%%% is solubilized during preparation of the algal chloroplasts. It acts in a catalytic fashion and appears to function in the electron transport chain which interconnects the two photosystems of photosynthesis. Euglena %%%cytochrome%%%-552 is most effective in restoration of NADP photoreduction activity; some restoration is observed with another algal c-type %%%cytochrome%%%, %%%Porphyra%%% %%%tenera%%% %%%cytochrome%%% -553. In contrast, restoration was not observed with either Euglena %%%cytochrome%%%-556 or horse-heart %%%cytochrome%%% c. ABSTRACT AUTHORS: Authors

2/7/8
DIALOG(R)File 5:Biosis Previews(R)

0001689681 BIOSIS NO.: 19664700093783
Energy- and electron-transfer systems in algal photosynthesis. I. Actions of two photochemical systems in oxidation-reduction reactions of %%%cytochrome%%% in %%%Porphyra%%%
AUTHOR: NISHIMURA MITSUO; TAKAMIYA ATUSI
AUTHOR ADDRESS: Johnson Res. Found., Univ. Penn., Philadelphia, Penn., USA
JOURNAL: BIOCHIM BIOPHYS ACTA 120 ((1)): p45-56 1966 1966
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: The light-induced oxidation-reduction reactions of %%%Porphyra%%% %%%cytochrome%%%-553 in the living thalli and isolated particles of three species of %%%Porphyra%%% (P. yezoensis, P. %%%tenera%%% and P. suborbiculata) were studied. The action spectrum of %%%cytochrome%%% oxidation had a maximum at 685-690 m.[mu] In the presence of background illumination of 680-700 m[mu], photochemical reduction by a second light of wavelengths shorter than 650 m[mu]. was observed. The maxima of the action spectrum for the reduction were located at 565 m[mu] and 615-620 m[mu]. This reduction of %%%cytochrome%%% by light absorbed by phycobilins was inhibited by 5-bromo-3- isopropyl-6-methyluracil, 3(4[image]-chlorophenyl)-1, 1-dimethylurea, 2-chloro-4, 6-bis-(ethylamino)-1, 3, 5-triazine, 3, 4-dichloropropionanilide and o-phenanthroline. These substances neither inhibited the light-induced oxidation of %%%cytochrome%%%, nor the dark reduction of %%%cytochrome%%% . In the presence of these substances, light-induced oxidation of %%%cytochrome%%% was observed on illumination of the light absorbed by phycobilins as well as by chlorophyll a. Effects of incident light intensity, dark period, inhibitors, gas phase, etc. on the rates and the steady-state change of the %%%cytochrome%%% reactions were investigated. Comparison of the observed amounts of %%%cytochrome%%% change and the amounts of %%%cytochrome%%%-553 extracted from the thalli indicated that the major portion of the %%%cytochrome%%%-553 present in the thalli changed its oxidation-reduction state on illumination. The quantum yield of %%%cytochrome%%% oxidation by light absorbed by chlorophyll a was about 0. 14. In the presence of 5-bromo-3-isopropyl-6-methyluracil, quantum yields with light absorbed by chlorophyll a and with light absorbed by phycobilins were about 0. 15 and 0. 11, respectively.
ABSTRACT AUTHORS: Authors

2/7/9
DIALOG(R)File 5:Biosis Previews(R)

0001140144 BIOSIS NO.: 19613600050054
Studies on algal %%%cytochrome%%%. II. Physico-chemical properties of crystalline %%%Porphyra%%% %%%tenera%%% %%%cytochrome%%% 553
AUTHOR: KATOH SAKAE
AUTHOR ADDRESS: U. Tokoy, Japan
JOURNAL: PLANT AND CELL PHYSIOL 1 ((2)): p91-98 1960 1960
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ordered

ABSTRACT: The physico-chemical properties of an algal %%%cytochrome%%%, P. %%%tenera%%% %%%cytochrome%%% 553 were investigated, using a crystalline preparation of the substance. The %%%cytochrome%%% was found to be highly resistant to heat and preservation. The stability of the %%%cytochrome%%% was also prominent in a wide range of pH. Absorption spectra as well as data concerning the extinction coefficients of the oxidized and reduced forms are presented. The oxidation-reduction potential of the %%%cytochrome%%% was determined at various pH. The value for the normal potential was found to decrease gradually with increasing pH, from 355mV at pH 5.0, to 270mV at pH 11.0. Electrophoretic investigation revealed that this %%%cytochrome%%% is a markedly acidic protein, with an isolectric point of pH 3.5. The molecular weight of the %%%cytochrome%%%

was determined from ultracentrifugal and diffusion experiments to be 13,600. The values for the minimum molecular weight calculated from the heme- and iron-contents are, respectively, 12,000 and 11,000. ABSTRACT AUTHORS: Author

2/7/10
DIALOG(R)File 5:Biosis Previews(R)

0001140141 BIOSIS NO.: 19613600050051
Some properties of %%%cytochrome%%% C from %%%Porphyra%%% %%%tenera%%%
AUTHOR: HASHIMOTO K; MASUHIRO I
JOURNAL: BULL JAPANESE SOC SCI FISH 25 ((7/9)): p561-564 1959 1959
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: %%%Cytochrome%%% c (Cyt) was purified from the alga. The preparation, containing 0.474% iron, proved to be electrophoretically homogeneous at various pH> s. The visible absorption spectra of the Cyt showed distinguishing characteristics, especially in the reduced form in 0.1 [image] acetate buffer of pH 6.0, the extinction coefficient of [alpha] maximum (at 553 m[mu]) was only about 3/4 of that of vertebrate %%%cytochrome%%%. In addition the whole spectrum shifted towards longer wave lengths than that of vertebrate Cyt; in 0.2 [image] NaOH, the whole spectrum was similar to that of vertebrates, both in positions and in extinction coefficients of maxima or minimum, and the extinction coefficient of a maximum was higher than that in the acetate buffer. Such a large difference of spectrum caused by change in pH has not been reported for %%%cytochrome%%% from any source. The pH-mobility curve of this protein also differed considerably from that of the horse. The isoelectric point was found to be around pH 4, which forms a marked contrast to vertebrate %%%cytochrome%%% (above pH 10). ABSTRACT AUTHORS: G. Gunter

2/7/11
DIALOG(R)File 5:Biosis Previews(R)

0001140087 BIOSIS NO.: 19613600049997
Studies on algal %%%cytochrome%%%. I. Enzymic activities pertaining to %%%Porphyra%%% %%%tenera%%% %%%cytochrome%%% 553 in cell-free extracts
AUTHOR: KATOH SAKAE
AUTHOR ADDRESS: U. Tokyo, Japan
JOURNAL: PLANT AND CELL PHYSIOL 1 ((1)): p29-38 1959 1959
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ordered

ABSTRACT: Enzymic activities pertaining to P. %%%tenera%%% cyto-chrome 553 were investigated with cell-free extracts of a red alga, P. %%%tenera%%%, and various fractions prepared therefrom. The algal extracts were found to be incapable, in the dark, of catalyzing oxidation of reduced %%%cytochrome%%% 553 at a rate sufficient to account for the respiratory oxygen-uptake in the intact cell. Oxidation of %%%cytochrome%%% 553 was

highly accelerated on illumination. The former reaction was found to be cyanide-sensitive and the latter, cyanide-insensitive. Both activities were found to be localized in the particulate fraction of the cell extract. Significant activities of reduced pyridine nucleotide-%%%cytochrome%%% reductase were discovered in the soluble fraction of the cell extract, the reaction being 2 or 3 times faster with TPNH than with DPNH as electron donor. There was no reaction with succinate in the presence of %%%cytochrome%%% and 2,6-dichlorophenol indophenol. P. %%%tenera%%% %%%cytochrome%%% 553 was shown to be localized in the plastids of the algal cell. Possible functions of %%%cytochrome%%% 553 in the algal metabolism are discussed. ABSTRACT AUTHORS: Author

2/7/12
DIALOG(R)File 5:Biosis Previews(R)

0001060132 BIOSIS NO.: 19603500042571
Crystallization of an algal %%%cytochrome%%%, %%%Porphyra%%% %%%tenera%%%-%%%cytochrome%%% 553
AUTHOR: KATOH SAKAE
AUTHOR ADDRESS: U. of Tokyo, Japan
JOURNAL: NATURE 186 ((4719)): p138-139 1960 1960
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

2/7/13
DIALOG(R)File 5:Biosis Previews(R)

0001042539 BIOSIS NO.: 19603500024974
Preparation of crystalline %%%cytochrome%%% from %%%Porphyra%%% %%%tenera%%%
AUTHOR: YAKUSHIJI EIJIRO; SUGIMURA YASUTOMO; SEKUZU ICHIRO; MORIKAWA ICHIRO ; OKUNUKI KAZUO
AUTHOR ADDRESS: Toho U., Narashino, Chiba, Japan
JOURNAL: NATURE 185 ((4706)): p105-106 1960 1960
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

? t s5/7/1-4

5/7/1
DIALOG(R)File 5:Biosis Previews(R)

17041661 BIOSIS NO.: 200300000380
Increasing the conformational stability by replacement of heme axial ligand in c-type cytochrome.
AUTHOR: Satoh Tadashi; Itoga Akito; Isogai Yasuhiro; Kurihara Masaaki; Yamada Seiji; Natori Miwa; Suzuki Noriko; Suruga Kohei; Kawachi Ryu; Arahira Masaomi; Nishio Toshiyuki; Fukazawa Chikafusa; Oku Tadatake

(Reprint)
AUTHOR ADDRESS: Department of Biological Chemistry, College of Bioresource Sciences, Nihon University, Kameino 1866, Fujisawa, Kanagawa, 252-8510, Japan**Japan
AUTHOR E-MAIL ADDRESS: oku@brs.nihon-u.ac.jp
JOURNAL: FEBS Letters 531 (3): p543-547 20 November, 2002 2002
MEDIUM: print
ISSN: 0014-5793
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: To investigate the role of the heme axial ligand in the conformational stability of c-type cytochrome, we constructed M58C and M58H mutants of the red alga %%%Porphyra%%% yezoensis %%%cytochrome%%% %%%c6%%% in which the sixth heme iron ligand (Met58) was replaced with Cys and His residues, respectively. The Gibbs free energy change for unfolding of the M58H mutant in water (DELTAGdegreeunf =1.48 kcal/mol) was lower than that of the wild-type (2.43 kcal/mol), possibly due to the steric effects of the mutation on the apoprotein structure. On the other hand, the M58C mutant exhibited a DELTAGdegreeunf of 5.45 kcal/mol, a significant increase by 3.02 kcal/mol compared with that of wild-type. This increase was possibly responsible for the sixth heme axial bond of M58C mutant being more stable than that of wild-type according to the heme-bound denaturation curve. Based on these observations, we propose that the sixth heme axial ligand is an important key to determine the conformational stability of c-type cytochromes, and the sixth Cys heme ligand will give stabilizing effects.

5/7/2

15877512 BIOSIS NO.: 200100049351
Structure of %%%cytochrome%%% %%%c6%%% from the red alga %%%Porphyra%%% yezoensis at 1.57 ANG resolution
AUTHOR: Yamada Seiji; Park Sam-Yong; Shimizu Hideaki; Koshizuka Yasutaka; Kadokura Kazunari; Satoh Tadashi; Suruga Kohei; Ogawa Masahiro; Isogai Yasuhiro; Nishio Toshiyuki; Shiro Yoshitsugu; Oku Tadatake (Reprint)
AUTHOR ADDRESS: Department of Biological Chemistry, College of Bioresource Sciences, Nihon University, 1866 Kameino, Fujisawa, Kanagawa, 252-8510, Japan**Japan
JOURNAL: Acta Crystallographica Section D Biological Crystallography 56 (12): p1577-1582 December, 2000 2000
MEDIUM: print
ISSN: 0907-4449
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The crystal structure of %%%cytochrome%%% %%%c6%%% from the red alga %%%Porphyra%%% yezoensis has been determined at 1.57 ANG resolution. The crystal is tetragonal and belongs to space group P43212, with unit-cell parameters a = b = 49.26 (3), c = 83.45 (4) ANG and one molecule per asymmetric unit. The structure was solved by the molecular-replacement method and refined with X-PLOR to an R factor of

19.9% and a free R factor of 25.4%. The overall structure of %%%cytochrome%%% %%%c6%%% follows the topology of class I c-type cytochromes in which the heme prosthetic group covalently binds to Cys14 and Cys17, and the iron has an octahedral coordination with His18 and Met58 as the axial ligands. The sequence and the structure of the eukaryotic red algal %%%cytochrome%%% %%%c6%%% are very similar to those of a prokaryotic cyanobacterial %%%cytochrome%%% %%%c6%%% rather than those of eukaryotic green algal c6 cytochromes.

5/7/3
DIALOG(R)File 5:Biosis Previews(R)

15369869 BIOSIS NO.: 200000088182
Crystallization and preliminary X-ray diffraction studies of %%%cytochrome%%% %%%c6%%% from %%%Porphyra%%% yezoensis
AUTHOR: Sasaki Tomokazu; Nakahara Megumi; Matsuda Aya; Yamasaki Takenobu; Katoh Sakae; Ohshima Shigeru; Oonishi Isao; Uchida Akira (Reprint)
AUTHOR ADDRESS: Department of Biomolecular Science, Toho University, Miyama 2-2-1, Funabashi, Chiba, 274-8510, Japan**Japan
JOURNAL: Acta Crystallographica Section D Biological Crystallography 56 (1): p79-80 Jan., 2000 2000
MEDIUM: print
ISSN: 0907-4449
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: %%%Cytochrome%%% %%%c6%%% from the red alga. %%%Porphyra%%% yezoensis has been purified and crystallized by the sitting-drop vapour-diffusion method. Two different crystal forms, tetragonal and orthorhombic, were obtained. The tetragonal crystals belong to space group P41212 or P43212, with unit-cell dimensions a = 49.33 (2), c = 83.70 (10) ANG. The orthorhombic crystals belong to space group P212121, with unit-cell dimensions a = 46.74 (2), b = 49.42 (1), c = 37.11 (1) ANG. Absorption spectra of the crystals showed that the tetragonal form was oxidized and the orthorhombic form was reduced.

5/7/4
DIALOG(R)File 5:Biosis Previews(R)

14283445 BIOSIS NO.: 199800077692
Ccs1, a nuclear gene required for the post-translational assembly of chloroplast c-type cytochromes
AUTHOR: Inoue Kairo; Dreyfuss Beth Welty; Kindle Karen L; Stern David B; Merchant Sabeeha; Sodeinde Ola A (Reprint)
AUTHOR ADDRESS: Dep. Biochem. Mol. Biol., Pennsylvania State Univ., University Park, PA 16802, USA**USA
JOURNAL: Journal of Biological Chemistry 272 (50): p31747-31754 Dec. 12, 1997 1997
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Nuclear genes play important regulatory roles in the biogenesis of the photosynthetic apparatus of eukaryotic cells by encoding factors that control steps ranging from chloroplast gene transcription to post-translational processes. However, the identities of these genes and the mechanisms by which they govern these processes are largely unknown. By using glass bead-mediated transformation to generate insertional mutations in the nuclear genome of Chlamydomonas reinhardtii, we have generated four mutants that are defective in the accumulation of the cytochrome b6f complex. One of them, strain abf3, also fails to accumulate holocytochrome c6. We have isolated a gene, Ccs1, from a C. reinhardtii genomic library that complements both the cytochrome b6f and %%%cytochrome%%% %%%c6%%% deficiencies in abf3. The predicted protein product displays significant identity with Ycf44 from the brown alga Odontella sinensis, the red alga %%%Porphyra%%% purpurea, and the cyanobacterium Synechocystis strain PCC 6803 (25-33% identity). In addition, we note limited sequence similarity with ResB of Bacillus subtilis and an open reading frame in a homologous operon in Mycobacterium leprae (11-12% identity). On the basis of the pleiotropic c-type cytochrome deficiency in the ccs1 mutant, the predicted plastid localization of the protein, and its relationship to candidate cytochrome biosynthesis proteins in Gram-positive bacteria, we conclude that Ccs1 encodes a protein that is required for chloroplast c-type holocytochrome formation.
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$159.87 Estimated cost File5
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$163.60 Estimated cost this search
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S7   20   (CYS()ALA()ALA()CYS)
S8   0   S7 AND HEME
S9   0   S7 AND HAEM
S10   0   S3 AND S7
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 3/7/50
DIALOG(R)File   5:Biosis Previews(R)

08166446   BIOSIS NO.: 198682012833
X-RAY DIFFRACTION ANALYSIS OF CYTOCHROME B-5 RECONSTITUTED IN EGG PHOSPHATIDYLCHOLINE VESICLES
AUTHOR: RZEPECKI L M (Reprint); STRITTMATTER P; HERBETTE L G
AUTHOR ADDRESS: DEPARTMENT BIOCHEMISTRY, UNIVERSITY CONNECTICUT HEALTH CENTER, FARMINGTON, CONN 06032, USA**USA
JOURNAL: Biophysical Journal 49 (4): p829-838 1986
ISSN: 0006-3495
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Cytochrome b5 was reconstituted asymmetrically into large unilamellar egg phosphatidylcholine vesicles. Asymmetry was preserved after sedimentation and partial dehydration to form oriented stacks of membranes. The periodicity of the centrosymmetric unit cell ranged between 145 and 175 .ANG., depending upon the water content of the oriented multilayer. X-ray diffraction data were collected to a resolution of 12 .ANG. and phase factors were unambiguously assigned by a swelling analysis to a resolution of 15 .ANG.. The lower-resolution profile structures clearly showed a highly asymmetric single membrane containing the %%%heme%%% %%%peptide%%% segment of the cytochrome on one side of the membrane bilayer. The higher-resolution data were also analyzed and profile structures were compared with various models for the distribution of cytochrome b5 nonpolar peptide within the membrane bilayer region. The data favor an asymmetric distribution of protein mass within the membrane bilayer.

 3/7/51
DIALOG(R)File   5:Biosis Previews(R)

08141509   BIOSIS NO.: 198681105400

THE USE OF A WATER-SOLUBLE CARBODIIMIDE TO STUDY THE INTERACTION BETWEEN CHROMATIUM-VINOSUM FLAVOCYTOCHROME C-552 AND CYTOCHROME C
AUTHOR: VIEIRA B (Reprint); DAVIDSON M; KNAFF D; MILLETT F
AUTHOR ADDRESS: DEPARTMENT OF CHEMISTRY, UNIVERSITY OF ARKANSAS, FAYETTEVILLE, ARKANSAS 72701, USA**USA
JOURNAL: Biochimica et Biophysica Acta 848 (1): p131-136 1986
ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The interaction between horse heart cytochrome c and Chromatium vinosum flavocytochrome c-552 was studied using the water-soluble reagent 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide (EDC). Treatment of flavocytochrone c-552 with EDC was found to inhibit the sulfide:cytochrome c reductase activity of the enzyme. SDS gel electrophoresis studies revealed that EDC treatment led to modification of carboxyl groups in both the Mr 21,000 %%%heme%%% %%%peptide%%% and the Mr 46,000 flavin peptide, and also to the formation of a cross-linked %%%heme%%% %%%peptide%%% dimer with an Mr value of 42000. Both the inhibition of sulfide:cytochrome c reductase activity and the formation of the %%%heme%%% %%%peptide%%% dimer were decreased when the EDC modification was carried out in the presence of cytochrome c. In addition, two new cross-linked species with Mr values of 34,000 and 59,000 were formed. These were identified as cross-linked cytochrome c-%%%heme%%% %%%peptide%%% and cytochrome c-flavin peptide species, respectively. Neither of these species were formed in the presence of a cytochrome c derivative in which all of the lysine amino groups had been dimethylated, demonstrating that EDC had cross-linked lysine amino groups on native cytochrome c to carboxyl groups on the heme and flavin peptides. A complex between cytochrome c and flavocytochrome c-552 was required for cross-linking to occur, since ionic strengths above 100 mM inhibited cross-linking.

3/7/52

07787566 BIOSIS NO.: 198580096461
INHIBITION OF LIPID PEROXIDATION BY HEME-NONAPEPTIDE DERIVED FROM CYTOCHROME C
AUTHOR: VODNYANSZKY L (Reprint); MARTON A; VENEKEI I; VEGH M; BLAZOVITS A; KITTEL A; HORVATH I
AUTHOR ADDRESS: SECOND INSTITUTE OF BIOCHEMISTRY, SEMMELWEIS UNIVERSITY MEDICAL SCHOOL, H-1444 BUDAPEST, HUNGARY**HUNGARY
JOURNAL: Biochimica et Biophysica Acta 835 (2): p411-414 1985
ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Heme-nonpeptide, derived from cytochrome c, inhibited the NADPH- and NADH-dependent lipid peroxidation of brain microsomes but, in the case of liver microsomes, this inhibitory effect manifested itself in the presence of SKF-525A [proadifen hydrochloride] (a specific blocker of cytochrome P-450) only. Heme-nonapeptide prevented the transient

accumulation of lipid peroxides in microsomes during lipid peroxidation. The O2 consumption of microsomes in the presence of NADPH or NADH was stimulated by heme-nonapeptide. There are 2 independent mechanisms of lipid peroxidation in liver microsomes. In vivo, the %%%heme%%%-%%%peptide%%%-sensitive mechanism, observed in brain microsomes, is more important.

3/7/53
DIALOG(R)File 5:Biosis Previews(R)

07747393 BIOSIS NO.: 198580056288
KINETICS OF DITHIONITE REDUCTION OF THE HEME NONAPEPTIDE OF CYTOCHROME C
AUTHOR: KAZMI S A (Reprint); MILLS M A; PITLUK Z W; SCOTT R A
AUTHOR ADDRESS: SCHOOL OF CHEMICAL SCIENCES, UNIVERSITY OF ILLINOIS, URBANA, ILL 61801, USA**USA
JOURNAL: Journal of Inorganic Biochemistry 24 (1): p9-12 1985
ISSN: 0162-0134
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

appears as 52

ABSTRACT: The kinetics of dithionite reduction of the oxidized heme nonapeptide fragment of horse heart cytochrome c were measured as a function of ionic strength at pH 7 and pH 9 by the stopped-flow technique. Dithionite concentration dependences indicate that the radical anion monomer, .**GRAPHIC**. is the active reductant. The pH 7 ionic strength dependence suggests that the %%%heme%%% %%%peptide%%% is reacting as a negatively charged molecule (its overall charge is calculated to be -1). Comparison of these results with the known rate of dithionite reduction of cytochrome c indicates that the heme nonapeptide has substantially greater inherent reactivity than cytochrome c, perhaps due to the greater accessibility of the heme.

3/7/54
DIALOG(R)File 5:Biosis Previews(R)

07730466 BIOSIS NO.: 198580039361
IDENTIFICATION OF THE BINDING SITE ON CYTOCHROME C-1 FOR CYTOCHROME C
AUTHOR: STONEHUERNER J (Reprint); O'BRIEN P; GEREN L; MILLETT F; STEIDL J; YU L; YU C-A
AUTHOR ADDRESS: DEPARTMENT CHEMISTRY, UNIVERSITY ARKANSAS, FAYETTEVILLE, ARKANSAS 72701, USA**USA
JOURNAL: Journal of Biological Chemistry 260 (9): p5392-5398 1985
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The reagent 1-ethyl-3-(3-[14C]trimethylaminopropyl)carbodiimide (ETC) was used to identify specific carboxyl groups on the horse heart cytochrome bc1 complex (ubiquinol-cytochrome c reductase, EC 1.10.2.2) involved in binding cytochrome c. Treatment of the cytochrome bc1 complex with 2 mM ETC led to inhibition of the electron transfer activity with

cytochrome c. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis indicated that both the cytochrome c1 %%%heme%%% %%%peptide%%% and the MW = 9175 hinge peptide were radiolabeled by ETC. In addition, a new band appeared at a position consistent with a 1:1 cross-linked cytochrome c1-hinge peptide species. Treatment of a 1:1 cytochrome bc1-cytochrome c complex with ETC led to the same inhibition of electron transfer activity observed with the uncomplexed cytochrome bc1, but to decreased radiolabeling of the cytochrome c1 %%%heme%%% %%%peptide%%%. Two new cross-linked species corresponding to cytochrome c-hinge peptide and cytochrome c-cytochrome c1 were formed in place of the cytochrome c1-hinge peptide species. To identify the specific carboxyl groups labeled by ETC, a purified cytochrome c1 preparation containing both the %%%heme%%% %%%peptide%%% and the hinge peptide was dimethylated at all the lysines to prevent internal cross-linking. The methylated cytochrome c1 preparation was treated with ETC and digested with trypsin and chymotrypsin, and the resulting peptides were separated by high pressure liquid chromatography. ETC labeled the cytochrome c1 peptides 63-81, 121-128 and 153-179 and the hinge peptides 1-17 and 48-65. All of these peptides are highly acidic and contain one or more regions of adjacent carboxyl groups. The only peptide consistently protected from labeling by cytochrome c binding was 63-81, demonstrating that the carboxyl groups at residues 66, 67, 76, and 77 are involved in binding cytochrome c. These residues are relatively close to the heme-binding cysteine residues 37 and 40 and indicate a possible site for electron transfer from cytochrome c1 to cytochrome c.

C-5-C

3/7/55
DIALOG(R)File 5:Biosis Previews(R)

07618285 BIOSIS NO.: 198579037184
DOMAIN STRUCTURE OF RABBIT HEMOPEXIN ISOLATION AND CHARACTERIZATION OF A HEME-BINDING GLYCOPEPTIDE
AUTHOR: MORGAN W T (Reprint); SMITH A
AUTHOR ADDRESS: DEP OF BIOCHEMISTRY, LOUISIANA STATE UNIV MED CENTER, NEW ORLEANS, LOUISIANA 70112, USA**USA
JOURNAL: Journal of Biological Chemistry 259 (19): p12001-12006 1984
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

C-5-C

ABSTRACT: Plasmin preferentially cleaves rabbit hemopexin at a single site, generating 2 nondisulfide-linked carbohydrate-containing fragments. In contrast, heme-hemopexin is almost totally resistant to this enzyme and is more resistant than the apoprotein to digestion by trypsin, chymotrypsin, papain, subtilisin and proteinase K as well. Plasmin digestion dramatically shortens the plasma clearance time of the molecule. The larger glycopeptide (I), shown to be derived from the amino terminus of the parent molecule by sequence analysis, has a MW near 35,000 with a pI [isoelectric point] of 5.0. It binds 1 mol of heme/mol in a manner analogous to intact hemopexin MW near 60,000 and pI 5.8. The smaller glycopeptide (II) has a MW near 25,000, a pI of 6.4, and does not bind heme. Of the 4 oligosaccharides of rabbit hemopexin, peptide I contains 3 oligosaccharides and peptide II contains 1. At micromolar concentrations, the 2 peptides migrate together during centrifugation

through sucrose gradients in the presence, but not in the absence, of %%%heme%%%. %%%Peptide%%% I has a far UV circular dichroism spectrum indicating it has some .alpha.-helical and extensive nonrepeating peptide structures whereas peptide II appears to be almost exclusively in a .beta.-sheet conformation. Peptide II is responsible for most of the positive ellipticity at 231 nm of native apohemopexin, but the increase in ellipticity at 231 nm characteristic of heme-hemopexin is not seen when peptide I binds heme, even in the presence of peptide II.

3/7/56
DIALOG(R)File 5:Biosis Previews(R)

07434576 BIOSIS NO.: 198528073479
CHEMILUMINESCENT ASSAY OF LIPID PEROXIDE IN PLASMA USING CYTOCHROME C %%%HEME%%% %%%PEPTIDE%%%
AUTHOR: IWAOKA T (Reprint); TABATA F
AUTHOR ADDRESS: DEP CHEM, UNIV CALIFORNIA RIVERSIDE, RIVERSIDE, CALIF 92521, USA**USA
JOURNAL: Febs Letters 178 (1): p47-50 1984
ISSN: 0014-5793
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: ENGLISH

3/7/57
DIALOG(R)File 5:Biosis Previews(R)

07336276 BIOSIS NO.: 198478071683
AN ANALYSIS OF THE HYDROGEN PER OXIDE MEDIATED CROSS LINKING OF LENS CRYSTALLINS CATALYZED BY THE HEME UNDECA PEPTIDE FROM CYTOCHROME C
AUTHOR: BODANESS R S (Reprint); LECLAIR M; ZIGLER J S JR
AUTHOR ADDRESS: LAB VISION RES, NATL EYE INST, NATL INST HEALTH, BUILD 6, ROOM 235, BETHESDA, MD 20205, USA**USA
JOURNAL: Archives of Biochemistry and Biophysics 231 (2): p461-469 1984
ISSN: 0003-9861
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: In contrast to other tissues, the lens exists in a milieu containing relatively high (micromolar) concentrations of H2O2. Activation of H2O2 to more-potent oxidant species via the heme-undecapeptide from cytochrome c produces alterations in lens crystallin polypeptides similar to the changes found in cataract. These include crystallin polypeptide crosslinking and the development of a blue fluorescence not attributable to tryptophan. Of the 3 classes of mammalian crystallins, .gamma.-crystallin is crosslinked by %%%heme%%% %%%peptide%%%-H2O2, whereas .alpha. and .beta. are not. %%%Heme%%%-%%%peptide%%% plus H2O2 generates dityrosine from free tyrosine, and, concomitant with crosslinking, the .gamma.-crystallin exposed to this system develops a new fluorophor with the characteristics of dityrosine. The findings with bovine and human crystallins are identical in this regard. In addition to the oxidation of tyrosine, exposure to %%%heme%%%

%%%peptide%%%-H2O2 results in the oxidation of tryptophan. The intrinsic fluorescence of .alpha., .beta. and .gamma.-crystallins is due primarily to tryptophan, and the intrinsic fuorescence of each is decreased by %%%heme%%% %%%peptide%%%-H2O2. Tryptophan oxidation occurs in all crystallins, but crosslinking occurs only in .gamma.-crystallin and is associated with oxidation of tryosine.

3/7/58
DIALOG(R)File 5:Biosis Previews(R)

07313272 BIOSIS NO.: 198478048679
KINETICS OF ELECTRON TRANSFER BETWEEN CARDIAC CYTOCHROME C-1 AND C/
AUTHOR: KIM C H (Reprint); BALNY C; KING T E
AUTHOR ADDRESS: DEP CHEM, STATE UNIV NY, ALBANY, NY 1222, USA**USA
JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 81 (7): p2026-2029 1984
ISSN: 0027-8424
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Highly purified cytochrome c1, which consists only 1 %%%heme%%% %%%peptide%%% and does not form a stable c1-c complex (c1-H-c complex), was used in studies of electron transfer between cytochromes c1 and c. A stable and ionic-strength-sensitive c1-c complex (i.e., the c1-H-c complex) in the forms of the various oxidation states apparently is not required, in contrast to the current belief of the participation of the complex in the electron transfer between cytochromes c1 and c. A minimum mechanism for electron transfer between these 2 cytochromes is suggested in accord with the experimental results.

3/7/59
DIALOG(R)File 5:Biosis Previews(R)

07313268 BIOSIS NO.: 198478048675
COVALENT CROSS LINKING OF THE ACTIVE SITES OF VESICLE BOUND CYTOCHROME B-5 AND NADH CYTOCHROME B-5 REDUCTASE
AUTHOR: HACKETT C S (Reprint); STRITTMATTER P
AUTHOR ADDRESS: DEP BIOCHEMISTRY, UNIV CONN HEALTH CENTER, FARMINGTON, CONN 06032, USA**USA
JOURNAL: Journal of Biological Chemistry 259 (5): p3275-3282 1984
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A water-soluble carbodiimide was used to promote the formation of amide bonds between carboxyl residues on cytochrome b5 and lysyl residues on [bovine liver] cytochrome b5 reductase. The visible and UV absorption spectrum of the purified cross-linked complex was identical with the sum of the spectra of the individual enzymes, and the average apparent MW of the complex, determined by sodium dodecyl sulfate-gel electrophoresis, was within 12% of the sum of the apparent MW of the 2 monomeric enzymes,

indicating that the cross-linked derivative was a dimer containing b5 reductase. When reconstituted into phospholipid vesicles, the amphipathic derivative showed substantially reduced Vmax values with the soluble electron acceptors potassium ferricyanide, cytochrome b5 %%%heme%%% %%%peptide%%% and cytochrome c, and with the membrane-bound acceptors amphipathic cytochrome b5 and stearyl-CoA desaturase. The soluble catalytic fragment of the derivative, produced by limited digestion with subtilisin Carlsberg, showed similar decreases in Vmax values with the above soluble acceptors. In contrast, intradimer electron transfer in the soluble fragment, measured by stopped flow spectrophotometry at 2.degree. C was very efficient. Ninety per cent of the cytochrome b5 in the derivative was reduced with a first order rate constant of 51 s-1 upon the addition of NADH; the transfer of electrons from NADH to the reductase FAD prosthetic group, which is the rate-limiting step in the reductase reaction mechanism, proceeded with an apparent rate constant of 57 s-1 under these conditions. These kinetic data show that the enzymes in the complex are cross-linked together at the surfaces involved in protein-protein contacts during electron transfer in an orientation similar to that assumed during electron transfer between the free proteins.

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DIALOG(R)File 5:Biosis Previews(R)

07262571 BIOSIS NO.: 198477094482
CYTOCHROME C-1 FROM PARACOCCUS-DENITRIFICANS
AUTHOR: LUDWIG B (Reprint); SUDA K; CERLETTI N
AUTHOR ADDRESS: INST BIOCHEM MED HOCHSCHULE LUEBECK, RATZEBURGER ALLEE D-2400 LUEBECK, FRG**WEST GERMANY
JOURNAL: European Journal of Biochemistry 137 (3): p597-602 1983
ISSN: 0014-2956
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Cytochrome c1 was purified from P. denitrificans. It is an acidic, hydrophobic polypeptide with an apparent MW of .apprx. 65,000 and a single, covalently attached heme; it cross-reacts immunologically with cytochrome c1 from yeast mitochondria. The amino acid sequence of the tryptic %%%heme%%% %%%peptide%%% of the bacterial cytochrome c1 shows extensive homology to the corresponding region of beef heart cytochrome c1. Positive evidence for a stable association of the Paracoccus cytochrome c1 with other polypeptides and b-type heme components (bc1-complex) was not yet obtained.

3/7/61
DIALOG(R)File 5:Biosis Previews(R)

06988167 BIOSIS NO.: 198376079602
THE HYDROGEN PER OXIDE MEDIATED OXIDATION OF NADPH TO NADP CATALYZED BY THE HEME UNDECA PEPTIDE FROM CYTOCHROME C
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AUTHOR ADDRESS: LAB VISION RESEARCH, NATL EYE INST, BUILD 6, ROOM 235,

BETHESDA, MD, USA**USA
JOURNAL: Biochemical and Biophysical Research Communications 113 (2): p 710-716 1983
ISSN: 0006-291X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: NAD(P)H is known to be oxidized by singlet molecular oxygen, perhydroxyl radical and hydroxyl radical. In marked contrast to these reactive oxygen species, NAD(P)H is stable in the presence of micromolar concentrations of H2O2. NADPH is rapidly oxidized by H2O2 in the presence of a %%%heme%%%-%%%peptide%%%. The oxidation product is enzymatically active NADP. In the absence of NADPH, the %%%heme%%%-%%%peptide%%% undergoes rapid degradation via reaction with H2O2. In the presence of NADPH, the reduced nucleotide is oxidized to NADP and the %%%heme%%%-%%%peptide%%% is partially protected from oxidation. Under certain conditions the reduced nucleotides may contribute to the protection of intracellular heme moieties from degradation engendered by endogenous or exogenous H2O2.

3/7/62
DIALOG(R)File 5:Biosis Previews(R)

06926450 BIOSIS NO.: 198376017885
THE INTERACTION BETWEEN HEME AND PROTEIN IN CYTOCHROME C-1
AUTHOR: TERVOORT M J (Reprint); VAN GELDER B F
AUTHOR ADDRESS: LAB BIOCHEMISTRY, BCP JANSEN INSTITUTE, UNIV AMSTERDAM, PO BOX 20151, 1000 HD AMSTERDAM**NETHERLANDS
JOURNAL: Biochimica et Biophysica Acta 722 (1): p137-143 1983
ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The optical spectrum of reduced bovine [heart] cytochrome c1 at 77.degree. K shows a fine splitting of the .beta.-band, which is indicative of the native conformation of the protein. At room temperature, this conformation is reflected in an absorbance band at 530 nm. The exposure of the heme of ferrocytochrome c1, investigated by solvent-perturbation spectroscopy, appears to be extremely sensitive to temperature and SH reagents, bound to the oxidized protein. Addition of combinations of potential ligands to the isolated tryptic %%%heme%%% %%%peptide%%% of cytochrome c1 reveals that only a mixture of methionine and cysteine (or their equivalents) generates a .beta.-band at 77.degree. K which is identical in shape to that of native cytochrome c1. In the EPR spectrum of a complex of ferrocytochrome c1 and nitric oxide at pH 10.5, no hyperfine splitting derived from a second ligated N atom could be detected. The results indicate that methionine and cysteine are the axial ligands of heme in cytochrome c1. The EPR spectrum of isolated ferricytochrome c1 is that of a low-spin heme iron compound with a gz value of 3.36 and a gy value of 2.04.

3/7/63

DIALOG(R)File 5:Biosis Previews(R)

06858256 BIOSIS NO.: 198375042199
TRANS NEURONAL UPTAKE OF HORSERADISH PEROXIDASE IN THE CENTRAL NERVOUS SYSTEM OF DIPTEROUS INSECTS
AUTHOR: NASSEL D R (Reprint)
AUTHOR ADDRESS: DEP ZOOL, UNIV LUND, HELGONAVAGEN 3, S-223 62 LUND, SWEDEN **SWEDEN
JOURNAL: Cell and Tissue Research 225 (3): p639-662 1982
ISSN: 0302-766X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Horseradish peroxidase (HRP) applied to lesioned neurons in the retina and thoracic ganglia of the flies Musca, Calliphora and Drosophila labeled axon terminals, dendrites and perikarya of the severed neurons after anterograde or retrograde passage. In addition, HRP reaction product secondarily labeled intact neurons that are contiguous with injured nerve cells. In many cases labeling of optic lobe neurons remote from primarily filled ones was also seen (here called tertiary labeling). HRP labeling was extensive and both primarily and transneuronally filled neurons could be resolved in almost as much detail as Golgi-impregnated or cobalt-silver-labeled cells. EM showed that in both primarily and secondarily filled neurons, reaction product was distributed diffusely in the cytoplasm. Transneuronal uptake of HRP was specific to certain types of neurons in the brain and thus displayed certain pathways. The pathways resolved by transneuronal labeling with HRP extend from the optic lobes to the thoracic ganglia and include visual neurons previously identified electrophysiologically and anatomically. Transneuronal HRP uptake, although believed to occur in vivo, could not be shown to be dependent on synaptic activity. Three other heme peptides tested were taken up by injured neurons, but showed no transneuronal labeling: lactoperoxidase, cytochrome c and microperoxidase.

3/7/64
DIALOG(R)File 5:Biosis Previews(R)

06826825 BIOSIS NO.: 198375010768
LYMPHOCYTE SPECIFICITY TO PROTEIN ANTIGENS 5. CONFORMATIONAL DEPENDENCE OF ACTIVATION OF CYTOCHROME C SPECIFIC T CELLS
AUTHOR: BUCHMUELLER Y (Reprint); CORRADIN G
AUTHOR ADDRESS: INST DE BIOCHIMIE, UNIV DE LAUSANNE, CH-1066 EPALINGES, SWITZ**SWITZERLAND
JOURNAL: European Journal of Immunology 12 (5): p412-416 1982
ISSN: 0014-2980
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Variations in the immunogenic and antigenic properties of native and denatured forms of cytochrome c were observed depending on the strain of mouse tested. In C57BL/6 and (C57BL/6 .times. DBA/2)F1 (BDF1) mice, priming with either native or denatured cytochrome c (apocytochrome c)

gave rise to T cell blasts responding in a similar fashion to the 2 forms of the antigen and to different peptides derived from CNBr cleavage of the protein when tested for proliferation in the presence of C57BL/6 or BDF1 accessory cells. A different pattern of proliferation was observed when apocytochrome c-specific DBA/2 or BDF1 T cell blasts were tested with DBA/2 accessory cells. In this case, no response was obtained to %%%heme%%% %%%peptide%%% 1-65. This was not due to an inability of DBA/2 macrophages to process and present %%%heme%%% %%%peptide%%% 1-65, as they were able to present this antigen to native cytochrome c-specific BDF1 T cell blasts. Thus, it seems that different sets of clones are generated upon priming BDF1 mice with denatured cytochrome c which are able to recognize different sets of peptides depending on the nature of the accessory cells. Degradation and presentation of native and denatured cytochrome c by macrophages apparently is dependent on the 3-dimensional conformation of the protein.

3/7/65
DIALOG(R)File 5:Biosis Previews(R)

06571082 BIOSIS NO.: 198273075009
THE EFFECT OF METHYLATION ON CYTOCHROME C FRAGMENT COMPLEMENTATION
AUTHOR: BREMS D N (Reprint); STELLWAGEN E
AUTHOR ADDRESS: THE DEP OF BIOCHEMISTRY, UNIV OF IOWA, IOWA CITY, IOWA 52242, USA**USA
JOURNAL: Journal of Biological Chemistry 256 (22): p11688-11690 1981
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The heme propionates of %%%heme%%% %%%peptide%%% 1-25 from horse heart cytochrome c were methylated in acidified methanol. The methylated %%%heme%%% %%%peptide%%% combines with apocytochrome c in a single 2nd order kinetic phase whose rate constant is within a factor of 4 of that measured for the unmethylated %%%heme%%% %%%peptide%%%. The Kd for the the 2 complexes are also within a factor of 4. The methylated and unmethylated complexes exhibit similar fluorescence quenching, far UV dichroic spectra and catalytic activities. The methylated complex has a Tm [melting temperature] about 10.degree. C lower than that of the unmethylated complex. The charge transfer band of the methylated complex occurs at 720 nm instead of 695 nm as observed for the unmethylated complex. Methylation of the outer heme propionate may cause a small steric effect which alters the geometry of the methionine 80 ligation with the heme Fe.

3/7/66
DIALOG(R)File 5:Biosis Previews(R)

06543294 BIOSIS NO.: 198273047221
QUANTITATIVE DATA ON PER OXIDATIC MARKERS FOR ELECTRON MICROSCOPY WITH A NOTE ON ACTIN IDENTIFICATION IN PARAMECIUM CELLS
AUTHOR: TIGGEMANN R (Reprint); PLATTNER H; RASCHED I; BAEUERLE P; WACHTER E
AUTHOR ADDRESS: FAC BIOL, UNIV KONSTANZ, D-7750 KONSTANZ, W GER**WEST

GERMANY
JOURNAL: Journal of Histochemistry and Cytochemistry 29 (12): p1387-1396 1981
ISSN: 0022-1554
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Several important points of %%%heme%%%-%%%peptide%%% cytochemistry were quantitatively analyzed, with particular regard to their use in EM immunocytochemistry. A simple procedure is presented for the preparation of heme-octapeptide (H-8-P) microperoxidase. H-8-P, heme-nonapeptide (H-9-P) and various horseradish peroxidase (HRP) isoenzymes were used for coupling with immunoglobulin (Ig) G or the papain-cleavage fragments from IgG (Fab) molecules. Ultracentrifugation and spectrophotometric analyses revealed the following characteristics of the conjugates; they are of a uniform size class, their diameters were calculated, and ranged from 5.6 (Fab-H-8-P; H-9-P) to 10.5 (IgG-HRP); the persistence of antigen binding capacity was ascertained; the deactivation of the marker peroxidase activity due to coupling was as low as 20-30%; optimal conditions for use of the EM with 3,3'-diaminobenzidine media were elaborated (with a pH optima somewhat different from some standard methods in current use); and on the basis of the quantitative data presented, an optimal compromise (either in favor of higher peroxidase activity with HRP conjugates or of smaller size with microperoxidase-Fab conjugates) can be achieved. The identification of isolated purified actin and of actin in cortical microfilament bundles and ciliary basal bodies of Paramecium cells served as a test object for the usefulness of conjugation products and optimized assay conditions for EM immunocytochemistry.

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DIALOG(R)File 5:Biosis Previews(R)

06542086 BIOSIS NO.: 198273046013
DIFFUSION CONTROLLED REACTION KINETICS OF THE BINDING OF CARBON MON OXIDE TO THE HEME UNDECA PEPTIDE OF CYTOCHROME C MICRO PEROXIDASE 11 IN HIGH VISCOSITY SOLVENTS
AUTHOR: HASINOFF B B (Reprint)
AUTHOR ADDRESS: DEP OF CHEM AND FAC OF MED, MEMORIAL UNIV OF NEWFOUNDLAND, ST JOHN'S, NEWFOUNDLAND A1B 3X7, CANADA**CANADA
JOURNAL: Archives of Biochemistry and Biophysics 211 (1): p396-402 1981
ISSN: 0003-9861
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The kinetics of the binding of CO to the covalently linked heme undecapeptide of [horse heart] cytochrome c (ferrous microperoxidase 11) were studied by flash photolysis in high-viscosity mixtures of glycerol:water, ethylene glycol:water and polyethylene glycol:water. This was done to examine the effects of diffusion-controlled ligand binding to a small %%%heme%%% %%%peptide%%% as a model for Hb and myoglobin. Arrhenius plots of the observed 2nd-order association rate constant are significantly curved consistent with a change from chemical activation

control at higher temperatures to diffusion control at the lowest temperatures and highest viscosities. The activation enthalpies in the diffusion-controlled region show a good correspondence with the solvent viscosity activation energies as predicted by theory. Depending upon the solvent, the deviation of the 2nd-order diffusion rate constants are 0.1-0.3 of that predicted from simple Smoluchowski theory for reaction between spheres of equal radii. Several models that ascribe these deviations to steric requirements are examined.

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DIALOG(R)File 5:Biosis Previews(R)

06511146 BIOSIS NO.: 198273015073
A STUDY OF THE ELECTRON TRANSFER PROPERTIES OF THE HEME UNDECA PEPTIDE FROM CYTOCHROME C BY PROTON NMR SPECTROSCOPY
AUTHOR: KIMURA K (Reprint); PETERSON J; WILSON M; COOKSON D J; WILLIAMS R J P
AUTHOR ADDRESS: INORGANIC CHEM LAB, SOUTH PARKS ROAD, OXFORD, ENGLAND, UK** UK
JOURNAL: Journal of Inorganic Biochemistry 15 (1): p11-26 1981
ISSN: 0162-0134
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: NMR spectroscopy was used to investigate the heme undecapeptide from [horse heart] cytochrome c. Assignments of resonances to specific residues were made based on spin decoupling, redox titration, and the pH and temperature dependence of resonance lines. An outline structure is presented based on the assignments, secondary shift data, and the X-ray crystal structure of cytochrome c. An equation is derived to relate the width of an NMR line during a redox titration to the percentage of each oxidation state. Using this equation the self-exchange rate constant for electron transfer for the %%%heme%%% %%%peptide%%% is 1.3 .times. 107 M-1 s-1 at 330.degree. K. Discussion of the self-exchange rate constants of cytochrome c, cytochrome c3 and cytochrome c551 is related to this constant for the heme undecapeptide.

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DIALOG(R)File 5:Biosis Previews(R)

05911740 BIOSIS NO.: 198069025727
SPECIFIC COVALENT LABELING OF CYTOCHROME P-450-CAM WITH 1-4 AZIDOPHENYL IMIDAZOLE AN INHIBITOR DERIVED PHOTO AFFINITY PROBE FOR P-450 HEME PROTEINS
AUTHOR: SWANSON R A (Reprint); DUS K M
AUTHOR ADDRESS: EDWARD A DOISY DEP BIOCHEM, ST LOUIS UNIV MED SCH, ST LOUIS, MO 63104, USA**USA
JOURNAL: Journal of Biological Chemistry 254 (15): p7238-7246 1979
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A generally applicable photoaffinity labeling procedure for the active site of P-450 heme proteins was developed using 1-(4-azidophenyl)imidazole (API), a photolabile analog of the common inhibitor N-phenylimidazole. The binding of API to [Pseudomonas putida] P-450CAM (KD .apprx. 1 .mu.M) elicited a type II spectral shift of the Soret band. Irradiation of the protein.cntdot.ligand complex at 313 nm caused specific covalent binding. Under similar conditions affinity labeling of pancreatic RNase was negligible. Reconstitution experiments demonstrated that API attachment was accompanied by inhibition of camphor hydroxylation. At cytochrome P-450CAM concentrations up to 10 .mu.M and API concentrations up to a 9-fold molar excess of label over protein, covalent binding increased linearly with label concentration until saturation of a single site was reached at 114% incorporation of tritiated label. More concentrated protein solutions (40-50 .mu.M), however, engendered gradual specific labeling at a 2nd discrete site. Covalent incorporation of API substantially in excess of 100% was observed. The mono- and dilabeled protein derivatives were readily resolved by gel electrofocusing (pI [isoelectric point] 5.2 and 5.8). A small heme-bearing fragment was isolated by Sephadex G-75 chromatography (MW .apprx. 5.0-5.5 .times. 103) from API-labeled cytochrome P-450CAM after cyanogen bromide degradation. This %%%heme%%% %%%peptide%%% fraction contained .apprx. 80% of the heme of cytochrome P-450CAM and .apprx. 70% of the incorporated label; its Soret maximum was at 356 nm in contrast to dissociated heme (390 nm). No significant amount of heme or label was associated with any other BrCN fragment. The resolved mono- and dilabeled heme peptides (pI 4.2 and 4.8) contained all radiolabel associated with the %%%heme%%% %%%peptide%%% fraction. Thus, photocovalent API labeling of cytochrome P-450CAM occurred almost exclusively in the close vicinity of the heme. The binding sites of cytochrome P-450CAM for the heme group and both labels are encompassed in a tightly structured domain which can be released in the form of a small %%%heme%%% %%%peptide%%% by selective chemical cleavage.

05908808 BIOSIS NO.: 198069022795
CYTOCHROME B-5 REDUCTION BY NADPH CYTOCHROME P-450 REDUCTASE EC-1.6.2.4
AUTHOR: ENOCH H G (Reprint); STRITTMATTER P
AUTHOR ADDRESS: KY CENT ENERGY RES, IRON WORKS PIKE, LEXINGTON, KY 40578, USA**USA
JOURNAL: Journal of Biological Chemistry 254 (18): p8976-8981 1979
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The NADPH-cytochrome P-450 reductase of steer liver microsomes catalyzes a rapid NADPH-dependent reduction of cytochrome b5 in the presence of detergent (1500/min at 30.degree. C) or phospholipid vesicles (7000/min at 33.degree. C). Neither the trypsin-solubilized reductase nor the soluble cytochrome b5 %%%heme%%% %%%peptide%%% could substitute for the complete amphipathic proteins. The detergent-solubilized reductase and cytochrome b5 were shown to bind to artificial phospholipid vesicles.

NADPH-dependent stearyl-CoA desaturation could also be reconstituted in system containing detergent-solubilized cytochrome P-450 reductase, cytochrome b5, stearyl-CoA desaturase and phospholipid. The resulting activity was similar to that obtained in an NADH-dependent system using cytochrome b5 reductase. The 1st order rate constant for the NADPH-dependent reduction of cytochrome b5 in microsomes was 1.1/s at 33.degree. C. This is equivalent to an observed turnover of 5100 mol of cytochrome b5 reduced/min/mol of cytochrome P-450 reductase in these microsomes. Cytochrome P-450 reductase and the NADPH-dependent reduction of cytochrome b5 in microsomes were inactivated by treatment of the microsomes with N-ethylmaleimide. NADPH-dependent cytochrome b5 reduction was restored by the addition of the detergent-solubilized (but not the trypsin-solubilized) cytochrome of P-450 reductase. The pathway of electron transfer from NADPH to cytochrome b5 in microsomes may be via the NADPH-cytochrome P-450 reductase.

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DIALOG(R)File 5:Biosis Previews(R)

05901974 BIOSIS NO.: 198069015961
SEMI SYNTHETIC ANALOGS OF CYTOCHROME C RECONSTRUCTED FROM NATURAL AND SYNTHETIC PEPTIDES
AUTHOR: NIX P T (Reprint); WARME P K
AUTHOR ADDRESS: DEP BIOCHEM BIOPHYS, PA STATE UNIV, UNIVERSITY PARK, PA 16802, USA**USA
JOURNAL: Biochimica et Biophysica Acta 578 (2): p413-427 1979
ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A biologically active semisynthetic hybrid of horse heart cytochrome c was prepared by combining the %%%heme%%% %%%peptide%%% 1-65 (HP 1-65), prepared by CNBr cleavage of natural cytochrome c, with a semisynthetic peptide corresponding to positions 66-104. A fully protected synthetic peptide 66-79 was prepared by a modified solid phase peptide synthesis procedure and was converted to its N-hydroxysuccinimide ester. A peptide corresponding to residues 81-104 of cytochrome c was also isolated from the CNBr cleavage mixture and its .epsilon.-amino groups and tyrosyl hydroxyl group were protected selectively with the t-butyloxycarbonyl group. This partially protected peptide was reacted with t-butyloxycarbonyl methionine N-hydroxysuccinimide ester to give a derivative having methionine at position 80. This product was deprotected, purified and then t-butyloxycarbonyl groups were again introduced specifically on the .epsilon.-amino groups to give the peptide, Boc(Lys,Tyr)80-104. A semisynthetic peptide corresponding to residues 66-104 of cytochrome c was prepared by condensing the synthetic peptide 66-79 N-hydroxysuccinimide ester with t-butyloxycarbonyl (Lys,Tyr)80-104. The semisynthetic product was deprotected, purified and combined under anaerobic conditions with a %%%heme%%% %%%peptide%%%, HP 1-65, that was isolated from the products of CNBr cleavage of native cytochrome c. The reconstituted semisynthetic cytochrome c was purified by ion exchange chromatography and had the same O2 uptake activity as native cytochrome c when assayed in the succinate oxidase system.

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DIALOG(R)File 5:Biosis Previews(R)

05900280 BIOSIS NO.: 198069014267
TEMPERATURE DEPENDENT SPIN STATE EQUILIBRIUM IN AN AZIDE IRON III HEME OCTA PEPTIDE COMPLEX A MODEL SYSTEM FOR THE SPIN EQUILIBRIA OF IRON III HEME PROTEINS
AUTHOR: HUANG Y-P (Reprint); KASSNER R J
AUTHOR ADDRESS: DEP CHEM, UNIV ILL CHIC CIRCLE, CHICAGO, ILL 60680, USA** USA
JOURNAL: Journal of the American Chemical Society 101 (19): p5807-5810 1979
ISSN: 0002-7863
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The temperature dependence of the magnetic susceptibility of an azide-ferric heme octapeptide was investigated as a model for the temperature-dependent spin-state equilibria of ferric heme proteins. The shift in the 1H NMR signal of sodium 4,4-dimethyl-4-silapentanesulfonate (DSS) caused by the heme octapeptide was measured from 12 to 73.degree. C in an aqueous-ethylene glycol solution. Magnetic susceptibilities calculated from the shifts do not exhibit a simple Curie behavior as would be expected for a pure high-spin or low-spin system. The temperature dependence of the susceptibility is consistent with a thermal spin-state equilibrium: high spin (S = 5/2) .dblarw. low spin (S = 1/2). The equilibrium constant [K] is 9.4 at 25.degree. C. Thermodynamic values determined from a plot of ln K vs. 1/T are .DELTA.H.degree. = -16,300 J/mol (-3890 cal/mol) and .DELTA.S.degree. = -36.0 J/(mol .cntdot. K) (-8.6 cal/(mol .cntdot. K)). Suitable axial ligands to the heme Fe are sufficient to provide a model for heme proteins that exhibit thermal spin equilibria. Equilibrium and thermodynamic values for the %%%heme%%% %%%peptide%%% are compared to values for heme proteins to determine the effect of protein structure on the spin-state equilibrium.

3/7/73
DIALOG(R)File 5:Biosis Previews(R)

05895244 BIOSIS NO.: 198069009231
BINDING OF CYTOCHROME B-5 TO PHOSPHO LIPID VESICLES AND BIOLOGICAL MEMBRANES EFFECT OF ORIENTATION ON INTER MEMBRANE TRANSFER AND DIGESTION BY CARBOXY PEPTIDASE Y
AUTHOR: ENOCH H G (Reprint); FLEMING P J; STRITTMATTER P
AUTHOR ADDRESS: DEP BIOCHEM, UNIV CONN HEALTH CENT, FARMINGTON, CONN 06032, USA**USA
JOURNAL: Journal of Biological Chemistry 254 (14): p6483-6488 1979
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A method is described which allows the direct measurement of

intermembrane protein transfer. Using this method the transfer of [stear liver] cytochrome b5 from artificial phospholipid vesicles and biological membranes was examined. This method involves the incubation of small, sonicated phospholipid vesicles with either biological membranes or large unilamellar phospholipid vesicles and subsequent separation by gel filtration. Cytochrome b5 transfer was observed between large and small single bilayer vesicles when cytochrome b5 was bound to preformed egg phosphatidylcholine vesicles. The cytochrome b5 of microsomes, however, did not transfer to small vesicles; neither did cytochrome b5 reductase nor exogenous, bound cytochrome b5. No detectable protein was transferred when high salt-washed microsomes were mixed with small, sonicated vesicles. Similar results were obtained using mitochondria and nuclear membrane fragments. Integral membrane proteins in general do not readily undergo intermembrane transfer between biological membranes. The ability of cytochrome b5 to transfer from artificial membranes and not from biological membranes may reflect a different in the nature of the protein binding. A nontransferable form of cytochrome b5, which may represent the microsomal type of binding, was obtained when cytochrome b5 was bound to preformed vesicles of dimyristyl phosphatidylcholine or when cytochrome b5 was bound during the formation of phosphatidylcholine vesicles. A soluble, %%%heme%%% %%%peptide%%% fragment of cytochrome b5 was released when vesicles containing cytochrome b5 in the transferable form were incubated with carboxypeptidase Y. In contrast, the nontransferable form of cytochrome b5 in microsomes and artificial vesicles was not released by carboxypeptidase Y treatment. There are at least 2 possible orientations of cytochrome b5 in phospholipid bilayers and these orientations may result in either hindered or rapid intermembrane transfer.

3/7/74
DIALOG(R)File 5:Biosis Previews(R)

05761603 BIOSIS NO.: 198018000594
REVERSIBLE OXYGENATION OF FERRO PORPHYRINS IN A BI LAYER PHOSPHO LIPID
AUTHOR: VASILENKO I A (Reprint); USHAKOVA I P; RADYUKHIN V A; FILIPPOVICH E I; SEREBRENNIKOVA G A; EVSTIGNEEVA R P
AUTHOR ADDRESS: M V LOMONOSOV MOSC INST PRECIS CHEM TECHNOL, MOSCOW, USSR** USSR
JOURNAL: Doklady Biophysics 241 p126-129 1978
ISSN: 0012-4974
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: ENGLISH

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DIALOG(R)File 5:Biosis Previews(R)

05732078 BIOSIS NO.: 197968043577
THE AMINO-ACID SEQUENCE OF CYTOCHROME C-PRIME FROM THE PURPLE SULFUR BACTERIUM CHROMATIUM-VINOSUM
AUTHOR: AMBLER R P (Reprint); DANIEL M; MEYER T E; BARTSCH R G; KAMEN M D
AUTHOR ADDRESS: DEP MOL BIOL, UNIV EDINB, EDINBURGH EH9 3JR, SCOTL, UK**UK
JOURNAL: Biochemical Journal 177 (3): p819-824 1979

ISSN: 0264-6021
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: An amino acid sequence is proposed for the cytochrome c' from the photosynthetic purple sulphur bacterium C. vinosum strain D. It is a single polypeptide chain of 131 residues, with heme-attachment cysteine residues at positions 121 and 124. The results discredit an earlier report of a di-%%%heme%%% %%%peptide%%% sequence from this protein. The sequence belongs to the same class as the published Alcaligenes and Rhodospirillum rubrum cytochrome c' sequences, but the resemblance is not close.

3/7/76
DIALOG(R)File 5:Biosis Previews(R)

05677454 BIOSIS NO.: 197967066449
PURIFICATION AND PROPERTIES OF A PEPTIC %%%HEME%%% %%%PEPTIDE%%% FROM CYTOCHROME C-1
AUTHOR: HALLENBECK P (Reprint)
AUTHOR ADDRESS: SP SCI LAB, UNIV CALIF, BERKELEY, CALIF 94720, USA**USA
JOURNAL: Biochemical and Biophysical Research Communications 85 (1): p 234-241 1978
ISSN: 0006-291X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A novel purification procedure was devised to isolate a %%%heme%%% %%%peptide%%% from bovine [heart] cytochrome c1. The procedure was based on unique properties of some heme peptides and was capable of processing small quantities (.apprx. 100 nmol) of material with satisfactory yields. The dansyl reactions, 2-dimensional TLC and electrophoresis demonstrated that the peptide was reasonably homogenous. The amino acid composition and spectral characteristics indicate a high degree of similarity with the peptic %%%heme%%% %%%peptide%%% of bovine cytochrome c.

3/7/77
DIALOG(R)File 5:Biosis Previews(R)

05663463 BIOSIS NO.: 197967052458
BLOOD BRAIN BARRIER IN RATS TO THE %%%HEME%%% %%%PEPTIDE%%% MICRO PEROXIDASE
AUTHOR: VAN DEURS B (Reprint); AMTORP O
AUTHOR ADDRESS: ANAT DEP A, UNIV COPENH, 71 RAADMANDSGADE, DK 2200 COPENHAGEN N, DEN**DENMARK
JOURNAL: Neuroscience 3 (8): p737-748 1978
ISSN: 0306-4522
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The blood-brain barrier to the hemepeptide tracer microperoxidase (MW 1900) was examined in rats. Microperoxidase was introduced i.v. (Group II) or by ventriculo-cisternal perfusion (Group I). The renal arteries in the i.v. perfused rats were clamped causing hypotension in some experiments. Some rats receiving microperoxidase i.v. were made hypertensive for a few minutes with metaraminol (Group III). The brains were fixed with aldehydes by ventriculo-cisternal perfusion. Brain tissue surrounding the 3rd ventricle at a maximal depth of 1 mm was used. In all experiments in Group I and II the junctions between the endothelial cells were tight to microvasculature, mainly basal (contraluminal) vesicles after ventriculo-cisternal perfusion of microperoxidase (Group I), and luminal vesicles after i.v. perfusion of microperoxidase (Group II). Free vesicles with microperoxidase also occurred. No evidence for transendothelial transport of microperoxidase by vesicles was obtained in the rats perfused through the ventricles or in the i.v. perfused normo- or hypotensive rats (Group I and II). In the hypertensive rats (Group III) the endothelial junctions were also tight to microperoxidase, but in these rats microperoxidase was apparently transported by vesicles from blood to brain in some segments (arterioles) of the microvasculature. In some segments of the cerebral vascular endothelium there may exist a population of vesicles, where at least some are connected to the surface, but under normal and hypotensive conditions are not involved in transendothelial transport. Such vesicular transport of material can be induced by hypertension.

3/7/78
DIALOG(R)File 5:Biosis Previews(R)

05555079 BIOSIS NO.: 197917004074
%%%HEME%%% %%%PEPTIDE%%% FIBRINOGEN CONJUGATES AS ELECTRON MICROSCOPIC TRACERS
AUTHOR: SHAINOFF J R; GONDA S R
JOURNAL: Federation Proceedings 38 (3 PART 1): p997 1979
ISSN: 0014-9446
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

3/7/79
DIALOG(R)File 5:Biosis Previews(R)

05486605 BIOSIS NO.: 197968073096
MODIFICATION AND IDENTIFICATION OF CYTOCHROME B-5 CARBOXYL GROUPS INVOLVED IN PROTEIN PROTEIN INTERACTION WITH CYTOCHROME B-5 REDUCTASE
AUTHOR: DAILEY H A (Reprint); STRITTMATTER P
AUTHOR ADDRESS: DEP BIOCHEM, UNIV CONN HEALTH CENT, FARMINGTON, CONN 06032, USA**USA
JOURNAL: Journal of Biological Chemistry 254 (12): p5388-5396 1979
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Carboxyl groups of the %%%heme%%% %%%peptide%%% of [beef liver] cytochrome b5 were modified by using a water-soluble carbodiimide and either methylamine, glycine ethyl ester, or taurine as a nucleophile. The reaction was carried out under mild conditions, at pH 7.0, so that only a few of the 21 available carboxyl groups reacted. The kinetic data of the reaction indicate that 1 carboxyl group is more reactive than the others and it is not the heme propionate group. A single heme propionate side chain was modified by the time 6 carboxyls had reacted. Derivatives of the %%%heme%%% %%%peptide%%% that were modified with methylamine were produced and separated by ion exchange chromatography. A total of 5 individual species containing from 2-4 modified carboxyl groups were obtained and characterized to determine which residues had reacted. Only a single heme propionate and Glu 47, 48 and 52 were modified with methylamine. %%%Heme%%% %%%peptide%%% derivatives modified with glycine ethyl ester, with 2-8 carboxyl groups reacted, were also isolated, but the altered residues were not identified. %%%Heme%%% %%%peptide%%% derivatives, prepared by using either methylamine or glycine ethyl ester as the nucleophile, showed increasing apparent Km values as electron acceptors for cytochrome b5 reductase, i.e., the apparent Km values for the %%%heme%%% %%%peptide%%% of cytochrome b5 with 0, 2, 3, 4 and 5-8 modified carboxyl groups were 8, 30, 50, 80 and 250-300 .mu.M, respectively. In all cases, the Vmax values were the same as that of the unmodified cytochrome. In contrast, modification of carboxyl groups with taurine, in which there is charge retention but steric displacement by the intervening 4 atoms that separate the carboxyl oxygen and the sulfonate oxygen, resulted in a decrease in Vmax but no change in the apparent Km. It is proposed that cytochrome b5 interacts with NADH:cytochrome b5 reductase via complementary charge pair interactions involving cytochrome b5 side chain carboxyls of Glu 47, 48 and 52, the single exposed heme propionate and a fifth, as yet unidentified, side chain carboxyl group.

05485952 BIOSIS NO.: 197866072436
MICRO PEROXIDASE UPTAKE INTO THE RAT CHOROID PLEXUS EPITHELIUM
AUTHOR: DEURS B V (Reprint)
AUTHOR ADDRESS: ANAT DEP A, UNIV COPENH, 71 RADMANDSGADE, DK-2200 COPENHAGEN N, DEN**DENMARK
JOURNAL: Journal of Ultrastructure Research 62 (2): p168-180 1978
ISSN: 0022-5320
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Uptake, transport and diffusion of the %%%heme%%%-%%%peptide%%% tracer microperoxidase (MP; MW 1900) in the rat choroid plexus were studied. MP was perfused ventriculo-cisternally or i.v. The plexuses were fixed by ventriculo-cisternal perfusion of aldehydes, and tissue sections were incubated in a diaminobenzidine-H2O2 medium containing imidazole at pH 8.8. After i.v. administration MP was found in the connective tissue of the plexus. Basement membranes were heavily labeled, while intercellular spaces between epithelial cells exhibited only a little MP.

AUTHOR ADDRESS: DEP BIOCHEM, UNIV CONN HEALTH CENT, FARMINGTON, CONN 06032, USA**USA
JOURNAL: Journal of Biological Chemistry 252 (16): p5656-5660 1977
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: NADH-cytochrome b5 reductase [steer liver] readily binds to preformed phospholipid vesicles either below or above the phase transition temperature of the lipid and in the absence of detergents. The isolated vesicles are free of unbound reductase, and the lipid is present as small, closed bilayers (250-400 .ANG. in diameter) as indicated by gel filtration, density gradient centrifugation and internal volume measurements with [3H]glucose. The order of substrate specificity of the bound reductase is: ferricyanide= cytochrome b5 bound to reductase vesicles (100%) > cytochrome b5 %%%heme%%% %%%peptide%%% (13%) > unbound cytochrome b5 (4.5%) > cytochrome b,5 vesicles (0.1%). A specific orientation of cytochrome b,5 and reductase in the bilayer is probably required for optimal interaction. Protein transfer occurs between reductase vesicles and cytochrome b5 vesicles. The transfer is time-dependent (40-70% complete in 2 h), does not involve vesicle fusion, is more rapid at the phase transition temperature of the phospholipid and appears to require a fluid bilayer.

05100501 BIOSIS NO.: 197763021357
ELECTRON TRANSPORT SYSTEMS IN KINETOPLASTIDA
AUTHOR: HILL G C
JOURNAL: Biochimica et Biophysica Acta 456 (2): p149-193 1976
ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: Cyanide-sensitive trypanosomatids have an electron transport system which includes cytochromes b, c1, c, aa3, and coenzyme Q9. The cytochromes c present in trypanosomatids are atypical, with an .alpha.-peak from 555-558 nm in the reduced form. Only 1 cysteine residue is present in the %%%heme%%% %%%peptide%%% region linking the protein to the prosthetic group. The prosthetic group is probably a monosubstituted protoheme IX with 1 unsaturated vinyl group. Some cyanide-sensitive trypanosomatids (e.g. Trypanosoma mega, L. tarentolae) have demonstrated action spectral evidence for 2 terminal oxidases present, cytochrome aa3 and cytochrome o. A branched electron transport system has been proposed for cyanide-sensitive trypanosomatids, with cytochrome aa3 as 1 oxidase and cytochrome o as an alternative oxidase. Salivarian trypanosomes grown in culture initially develop succinate oxidation which is cyanide insensitive. Some insect trypanosomatids have a high percentage of succinate cyanide-insensitive oxidation e.g., T. mega with 50% KCN insensitivity. The identity of the oxidase which has an intermediate sensitivity to KCN in comparison to cytochrome aa3, or the L-.alpha.-glycerophosphate oxidase, is not known. Bloodstream forms of

African trypanosomes have a cyanide-insensitive L-.alpha.-glycerophosphate oxidase system. The system consists of 2 components, the particulate L-.alpha.-glycerophosphate dehydrogenase and the particulate L-.alpha.-glycerophosphate oxidase. The oxidase is inhibited by aromatic hydroxamic acids and the trypanocidal drug suramin.

3/7/84

04950874 BIOSIS NO.: 197662047013
THE AROMATIC AND HEME CHROMOPHORES OF RABBIT HEMOPEXIN DIFFERENCE ABSORPTION AND FLUORESCENCE SPECTRA
AUTHOR: MORGAN W T; SUTOR R P; MULLER-EBERHARD U
JOURNAL: Biochimica et Biophysica Acta 434 (2): p311-323 1976
ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: Spectrophotometric and fluorimetric techniques were employed to characterize the environment of the heme chromophore of rabbit hemopexin and to monitor changes in the environment of aromatic amino acid residues induced by the interaction of hemopexin with porphyrins and metalloporphyrins. Difference spectra showed maxima at 292 and 285 nm when hemopexin binds heme or deuteroheme but not deuteroporphyrin. These maxima are attributed to alterations in the local environment of tryptophan and tyrosine residues. Spectrophotometric titrations of the tyrosine residues of hemopexin, heme-hemopexin and hemopexin in 8 M urea showed apparent pK values at 11.4, 11.7 and 10.9, respectively. Perturbation difference spectra produced by 20% vol/vol ethylene glycol are consistent with the exposure of 6-8 of the 14 tyrosine residues and 6-8 of the 15 tryptophan residues of hemopexin to this perturbant. Only small differences were found between the perturbation spectra of apo- and heme-hemopexin near 290 nm, suggesting that slight or compensating changes in the exposure to solvent of tryptophan chromophores occur. In the Soret spectral region, the exposure of heme in the heme-hemopexin complex to ethylene glycol was 0.7, relative to the fully exposed %%%heme%%% %%%peptide%%% of cytochrome c. The fluorescence quantum yields of apo- and heme-hemopexin were estimated to be 0.06 and 0.03, respectively, compared to a yield of 0.13 for L-tryptophan. Iodide quenched 50% of the fluorescence of tryptophan residues in the apoprotein and 20% of the residual fluorescence of the deuteroheme-hemopexin complex. Cs was not effective quencher. Modification of approximately 4 tryptophan residues with N-bromosuccinimide also decreased the relative fluorescence of apo-hemopexin by 50% and concomitantly reduced the heme-binding ability of the protein by 70%. The existence of sterically unhindered tryptophan residues in either apo- or heme-hemopexin is unlikely since no charge transfer complexes between these proteins and N-methylnicotinamide were detected.

3/7/85

04648325 BIOSIS NO.: 197559054468
A TRYPSIN RESISTANT %%%HEME%%% %%%PEPTIDE%%% FROM CARDIAC CYTOCHROME C-1
AUTHOR: YU L; CHIANG Y-L; YU C-A; KING T E
JOURNAL: Biochimica et Biophysica Acta 379 (1): p33-42 1975
ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

3/7/86
DIALOG(R)File 5:Biosis Previews(R)

04531921 BIOSIS NO.: 197511038064
RECONSTITUTION OF HORSE HEART CYTOCHROME C KINETICS OF THE COMPLEX FORMATION PHASE
AUTHOR: MARKS R H L; HARBURY H A
JOURNAL: Federation Proceedings 34 (3): p604 1975
ISSN: 0014-9446
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

3/7/87
DIALOG(R)File 5:Biosis Previews(R)

04330348 BIOSIS NO.: 197410076503
THE OXIDATION OF CATECHOLAMINES BY %%%HEME%%% %%%PEPTIDE%%% OBTAINED FROM ENZYMATICALLY DIGESTED YEAST CYTOCHROME C
AUTHOR: MASUDA Y; TAKAHASHI K; MURANO T
JOURNAL: Japanese Journal of Pharmacology 24 (SUPPL): p120 1974
ISSN: 0021-5198
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

3/7/88
DIALOG(R)File 5:Biosis Previews(R)

04269189 BIOSIS NO.: 197410015344
CHEMISTRY OF TYPE C %%%HEME%%% %%%PEPTIDE%%% SYSTEMS
AUTHOR: MYER Y P; HARBURY H A
JOURNAL: Annals of the New York Academy of Sciences 206 p685-700 1973
ISSN: 007-8923
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

3/7/89
DIALOG(R)File 5:Biosis Previews(R)

04208005 BIOSIS NO.: 197356024447
PURIFICATION OF THE %%%HEME%%% %%%PEPTIDE%%% OF CYTOCHROME C BY AFFINITY CHROMATOGRAPHY
AUTHOR: WILCHEK M
JOURNAL: Analytical Biochemistry 49 (2): p572-575 1972
ISSN: 0003-2697
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

3/7/90
DIALOG(R)File 5:Biosis Previews(R)

04053869 BIOSIS NO.: 197309040346
A %%%HEME%%% %%%PEPTIDE%%% LABELED ANTIBODY FRAGMENT AS A MARKER FOR INTRA CELLULAR ANTIGENS
AUTHOR: KRAEHENBUHL J P; GALARDY R E; JAMIESON J D
JOURNAL: Federation Proceedings 32 (3 PART 1): p1027 1973
ISSN: 0014-9446
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

3/7/91
DIALOG(R)File 5:Biosis Previews(R)

04053484 BIOSIS NO.: 197309039961
A %%%HEME%%% %%%PEPTIDE%%% LABELED ANTIBODY FRAGMENT AS A MARKER FOR INTRA CELLULAR ANTIGENS
AUTHOR: KRAEHENBUHL J P; GALARDY R E; JAMIESON J D
JOURNAL: Federation Proceedings 32 (3 PART 1): p962 1973
ISSN: 0014-9446
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

3/7/92
DIALOG(R)File 5:Biosis Previews(R)

03388655 BIOSIS NO.: 197006075201
EXPERIMENTS ON THE SYNTHESIS AND SPECTRAL CHARACTERIZATION OF CYTOCHROME RELATED MOLECULES
AUTHOR: ROBINSON A B
JOURNAL: Dissertation Abstracts B Sciences and Engineering 29 (1): p146-B 1968
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

3/7/93
DIALOG(R)File 5:Biosis Previews(R)

03144780 BIOSIS NO.: 196905045621
INST PULSED PROTON MAGNETIC RESONANCE STUDIES OF CYTOCHROME C AND CYTOCHROME A %%%HEME%%% %%%PEPTIDE%%% ABSTRACT
AUTHOR: KOWALSKY A
JOURNAL: Federation Proceedings 28 (2): p603 1969
ISSN: 0014-9446
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

3/7/94
DIALOG(R)File 5:Biosis Previews(R)

03110997 BIOSIS NO.: 196905007569
AN OXIDATIVE EFFECT OF ENZ CYTOCHROME C %%%HEME%%% %%%PEPTIDE%%% SACCHAROMYCES-OVIFORMIS
AUTHOR: BABA Y; MIZUSHIMA H; WATANABE H
JOURNAL: Chemical and Pharmaceutical Bulletin (Tokyo) 16 (4): p763-764 1968
ISSN: 0009-2363
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

3/7/95
DIALOG(R)File 5:Biosis Previews(R)

0001789232 BIOSIS NO.: 19674800073237
The structural gene for yeast cytochrome C
AUTHOR: SHERMAN FRED; STEWART JOHN W; MARGOLIASH EMANUEL; PARKER JOHN; CAMPBELL WAYNE
AUTHOR ADDRESS: Univ. Rochester Sch. Med. and Dent., Rochester, N. Y., USA
JOURNAL: PROC NAT ACAD SCI USA 55 ((6)): p1498-1504 1966 1966
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: The primary structure of iso-1 -cytochrome c from baker's yeast is coded by the chromosomal gene CY1. This conclusion was reached by isolating a revertant, CY 1-2-a, from a mutant strain cy1-2 that specifically lacks iso-1-cyto chrome c. The sites of the original mutation and of the reversion are at the same genetic locus, and the revertant gene segregates from the wild-type gene in the expected 2 : 2 Mendelian fashion. The structure of the iso-1-cytochrome c isolatedfrom the revertant strain differs from that of the parental protein in the %%%heme%%% %%%peptide%%% region. This was shown by amino acid analyses of the intact proteins and the heme peptides, as well as by peptide maps of tryptic and chymotryptic digests. These results indicate that mitochondria do not contain all the genetic information coding for the

primary structures of all intramitochondrial proteins. ABSTRACT AUTHORS: Authors

3/7/96
DIALOG(R)File 5:Biosis Previews(R)

0001779391 BIOSIS NO.: 19674800063396
The reactivity of the lysyl residues of cytochrome bR
AUTHOR: OZOLS JURIS; STRITTMATTER PHILIPP
AUTHOR ADDRESS: Wash. Univ. Sch'. Med., Saint Louis, Missouri, USA
JOURNAL: J BIOL CHEM 241 ((20)): p4793-4797 1966 1966
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: The modification of [alpha]- and -amino groups in cytochrome b5 with acetic anhydride, succinic anhydride, and 2,4,6-trinitrobenzene 1-sulfonic acid (trinitrobenzene sulfonate) was described. Acylation of these residues increases the rate of heme dissociation from the protein in the presence of urea, without altering the spectrum or enzymatic reduction of the cytochrome. Trinitrophenylation of all of the a- and -amino groups results in a marked alteration of the protein structure. Even more extensive changes in the protein structure occurred when trinitrophenylation was carried out in the absence of the heme. The kinetics of trinitrophenylation showed that 3 of the lysyl residues in cytochrome b5 are particularly reactive. These residues are largely confined to the %%%heme%%% %%%peptide%%% core rather than to the lysyl residues near the amino- and carboxyl-terminal ends of the protein. Because the completely acetylated apocytochrime b5 recombines with heme to yield a cytochrome b5 recombines with heme to yield a cytochrome t5 with unaltered spectral properties, the a- and the -amino groups are not involved directly in either heme binding of the catalytic activity of cytochrome b5. ABSTRACT AUTHORS: Authors

3/7/97
DIALOG(R)File 5:Biosis Previews(R)

0001753404 BIOSIS NO.: 19674800037408
Complex formation between methionine and a %%%heme%%% %%%peptide%%% from cytochrome c
AUTHOR: HARBURY HENRY A; CRONIN JOHN R; FANGER MICHAEL W; HETTINGER THOMAS P; MURPHY ALEXANDER J; MYER YASH P; VINOGRADOV SERGE N
AUTHOR ADDRESS: Dep. Biochem., Yale Univ., New Haven, Conn., USA
JOURNAL: PROC NAT ACADSCI 54 ((6)): p1658-1664 1965 1965
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: N-Acetyl-DL-methionine, N-acetyl-DL-methionlne methyl ester, diethyl sulfide, and several other thioethers have been shown to form complexes with a heme octapeptide from horse heart cytochrome c, with a glutathione adduct of iron protoporphyrin IX, and, in a few instances tested, with iron protoporphyrin K itself. Binding in the peptide systems

occurs to the lower limit of the pH-range covered (pH2), is stronger in the reduced than in the oxidized state, and results in the appearance of hemochrome- and hemichrome-type spectra. The oxidation-reduction potential of the heme octapeptide in the presence of N-acetyl-DL-methionine is less negative than that of the imidazole-heme octapeptide system at pH 7. The possiblity is considered that methionine-heme binding might occur among the cytochromes c. ABSTRACT AUTHORS: Authors

3/7/98
DIALOG(R)File 5:Biosis Previews(R)

0001748160 BIOSIS NO.: 19674800032164
The restricted tryptic cleavage of cytochrome b5
AUTHOR: STRITTMATTER PHILIPP; OZOLS JURIS
AUTHOR ADDRESS: Wash. Univ. Sch. Med., Saint Louis, Missouri, USA
JOURNAL: J BIOL CHEM 241 ((20)): p4787-4792 1966 1966
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: Two major heme protein components have been identified in cytochrome b5 preparations from calf liver by electrophoresis and have been separated chromatographically. These 2 forms of cytochrome b5 differ in that one contains a carboxyl-terminal glutamylserine peptide sequence which is absent from the second. Tryptic digestion of either heme protein species yields the same core %%%heme%%% %%%peptide%%% by the cleavage of 2 peptides, one from the carboxyl-terminal and one from the amino-terminal end. The amino acid sequence of the small peptides released by trypsin and the peptide sequence in cytochrome b5 were determined. The core %%%heme%%% %%%peptide%%% contains 81 amino acid residues and is indistinguishable in its spectral and catalytic properties from the original cytochrome b5 preparations. This %%%heme%%% %%%peptide%%% thus provides the simplest unit for a complete analysis of the catalytic properties and the structure of cytochrome b5. ABSTRACT AUTHORS: Authors

3/7/99
DIALOG(R)File 5:Biosis Previews(R)

0001732441 BIOSIS NO.: 19674800016445
Optical rotatory dispersion of cytochrome c. II. Comparative data for A heme octapeptide
AUTHOR: MYER YASH P; HARBURY HENRY A
AUTHOR ADDRESS: Dep. Biochem., Yale Univ., New Haven, Conn., USA
JOURNAL: J BIOL CHEM 241 ((19)): p4299-4303 1966 1966
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: The optical rotatory dispersion of horse heart cytochrome c has been compared with that of model heme octapeptide systems. When one of the coordination positions about the heme iron of the peptide systems is

occupied by the imidazole side chain of the single histidine residue, dispersion curves are obtained which, in a number of respects, are similar to those of the intact protein. There are also, however, major differences. The most striking of these occur in the Soret region, where the patterns recorded for the peptide complexes resemble more nearly those for myoglobin and hemoglobin than those for horse heart cytochrome c. Only with the %%%heme%%% %%%peptide%%% in aggregated form were curves obtained which approach the pattern for the parent ferricytochrome molecule in the Soret region. Complexes of the oxidized %%%heme%%% %%%peptide%%% with extrinsic imidazole and with methionine derivatives yield curves which exhibit, in addition to the Cotton effects in the Soret region, a broad positive extremum in the range 500 to 600 m[mu], and multiple Cotton effects in the ultraviolet. Reduction of these complexes results in shifts of the curves to longer wave lengths in the Soret region, the appearance of well defined Cotton effects associated with the hemochrome bands near 520 and 550 m[mu], and extensive modification of the complicated pattern in the ultraviolet region. The curves obtained differ for the 2 oxidation states throughout the wave length range studied (220 to 620 m[mu]). Rotations recorded at wave lengths near 230 m[mu] are greater than those calculated for 8 residues in random coil form on the basis of relationships for simple polypeptides. This excess rotation is not diminished by the addition of 8 [image] urea, but is reduced greatly upon protonation or photooxidation of tFe histidine residue of the peptide. Such treatment leads also to loss of the large Cotton effect in the Soret region. ABSTRACT AUTHORS: Authors

3/7/100
DIALOG(R)File 5:Biosis Previews(R)

0001727487 BIOSIS NO.: 19674800011491
Optical rotatory dispersion of a %%%heme%%% %%%peptide%%% from cytochrome c
AUTHOR: ULMER DAVID D
AUTHOR ADDRESS: Peter Bent Brigham Hosp., Boston, Mass., USA
JOURNAL: PROC NAT ACAD SCI USA 55 ((4)): p894-899 1966 1966
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: The oxidized and reduced peptic %%%heme%%% %%%peptide%%% of [horse heart] cytochrome c generates extrinsic Cotton effects which closely resemble those of the intact protein. The intrinsic Cotton effect of the peptide is also similar in appearance to that of native cytochrome, but differs slightly in spectral position. The Cotton effects which arise from aromatic amlno acid chromophores in the intact protein are absent in the peptide, which contains no aromatic residues. The data suggest that both the magnitude and the general form of the extrinsic Cotton effects of cytochrome c are deterined by a small portion of the molecule[long dash]the %%%heme%%% %%%peptide%%% segment. The conformation of this segment, as it exists in native cytochrome, is apparently largely preserved in the isolated peptide. ABSTRACT AUTHORS: Author

3/7/101
DIALOG(R)File 5:Biosis Previews(R)

0001691842 BIOSIS NO.: 19664700095944
Tyrosine and tryptophan in cytochrome
AUTHOR: ULMER DAVID D
AUTHOR ADDRESS: Harvard Med. Sch., Boston, Mass., USA
JOURNAL: BIOCHEMISTRY 5 ((6)): p1886-1892 1966 1966
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: The optical rotatory dispersion of oxidized cytochrome c reveals distinct Cotton effect maxima at both 287 and 278 m [mu]; the peak at 278 M [mu] is absent in reduced cytochrome c (Ulmer, D. D. (1965), Biochemistry 4, 902]. The nature of the chromophore giving rise to the oxidation-reduction-dependent Cotton effect at 278 m [mu] was investigated by spectropolarimetric studies and chemical modifications of the oxidized and reduced proteins. Acetylimidazole modifies two tyrosyl residues in ferricytochrome c while less than one-half tyrosine is modified in the reduced cytochrome; however, acylation does not alter the optical rotatory dispersion, indicating that the oxidation-reduction-dependent Cotton effect does not arise from "free" tyrosyl groups. In contrast, titration with N-bromosuccinimide modifies one tryptophan, and, concomitantly, obliterates the peak at 278 m[mu] ; this suggests that the oxidation-reduction-dependent Cotton effect arises from the single tryptophyl residue of the horse heart protein. Such a conclusion is supported by studies of the optical rotatory dispersion of cytochromes isolated from different species, which vary in aromatic amino acid composition. Thus, tuna ferricytochrome, the only species having two trytophans, exhibits a Cotton effect with a peak at 278 m[mu] nearly double in magnitude that observed in any other cytochrome. Neither apocytochrome, from which the heme has been removed, nor a peptic %%%heme%%% %%%peptide%%% from cytochrome c, which lacks aromatic amino acids, exhibit Cotton effects in the spectral range 270-300 m[mu]. Moreover, the Cotton effects generated by aromatic residues of the native cytochrome are markedly sensitive both to alkaline pH and to iron-binding ligands known to alter the relationship of the heme to the protein. These data suggest that the asymmetric environment of aromatic chromophores in cytochrome c is dependent upon an interaction of the heme with regions of the primary structure containing aromatic amino acids; oxidation-reduction appears to affect the nature of this interaction.
ABSTRACT AUTHORS: Authors

3/7/102
DIALOG(R)File 5:Biosis Previews(R)

0001626657 BIOSIS NO.: 19664700030758
Trifluoroacetylated cytochrome c
AUTHOR: FANGER MICHAEL W; HARBURY HENRY A
AUTHOR ADDRESS: Dep. Biochem., Yale Univ., New Haven, Conn., USA
JOURNAL: BIOCHEMISTRY 4 ((11)): p2541-2545 1965 1965
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: The lysine residues of horse heart cytochrome c can be trifluoroacetylated by reaction with ethyl thioltrifluoroacetate and the blocking groups subsequently removed by mild alkaline hydrolysis. The regenerated material displays full electron-transfer activity in the succinate oxidase system and moves on Amberlite CG-50 in the same manner as fraction I of unmodified preparations. Trifluoroacetylated cytochrome c containing no amino groups detectable by dinitrophenyla-tion or treatment with nitrous acid is without activity in the succinate oxidase system, but displays, over the range of pH 6-10, Soret and visible spectra essentially inchanged from those of nontrif luoro-acetylated samples. By tryptic hydrolysis of the trifluoroacetylated protein, a %%%heme%%% %%%peptide%%% of 38 amino acid residues, representing approximately one-third of the cytochrome molecule, has been prepared. ABSTRACT AUTHORS: Authors

3/7/103
DIALOG(R)File 5:Biosis Previews(R)

0001179142 BIOSIS NO.: 19623700002034
Amino-acid sequence of a %%%heme%%% %%%peptide%%% with two heme groups
AUTHOR: DUS KARL; BARTSCH ROBERT G; KAMEN MARTIN D
AUTHOR ADDRESS: Brandeis U., Waltham, Mass.
JOURNAL: JOUR BIOL CHEM 236 ((8)): pPC47-PC48 1961 1961
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: Peptic digestion of the variant heme protein ("RHP"), as obtained from the photoanaerobe Chromatium, strain D, releases peptides which still retain both heme groups of the original protein in each peptide chain. When Celite column chromatography (with the solvent system: n-butanol, acetic acid, water) is used, two peptides are found as major components of the digest. Analysis of each peptide by further fragmentation with trypsin, chymotrypsin, papain, and protease, followed by separation of the fragment peptides using two-dimensional paper chromatography and high voltage electrophoresis, leads to a proposed sequence of amino acids, as follows: H2N[center dot]Phe[center dot]Ala[center dot]GlyLys[center dot]CysO3H[center dot]Ser[center dot]Glu[center dot]CysO3H[center dot]His[center dot]-Thr[center dot]Leu[center dot]Val[center dot]Ala[center dot]Asp[center dot]Glu[center dot]Gly Ser[center dot]Ala[center dot]Lys[center dot]CySO3H[center dot]His[center dot]Thr[center dot]Phe[center dot]Asp[center dot]-Glu[center dot]Gly[center dot]SerCOOH. This 27-amino residue chain contains both heme groups; one is attached, as in cytochrome C, to the cysteic acid residues (nos. 5 and 8 in the above chain) while the placement of the second is still uncertain. ABSTRACT AUTHORS: Authors

3/7/104
DIALOG(R)File 5:Biosis Previews(R)

0001054780 BIOSIS NO.: 19603500037218
Linked functions in heme systems: oxidation-reduction potentials and

absorption spectra of a %%%heme%%% %%%peptide%%% obtained upon peptic hydrolysis of cytochrome c
AUTHOR: HARBURY HENRY A; LOACH PAUL A
AUTHOR ADDRESS: Yale U., New Haven, Conn.
JOURNAL: PROC NATL ACAD SCI 45 ((9)): p1344-1359 1959 1959
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: Studies are reported of the oxidation-linked proton functions of a heme undecapeptide obtained upon peptic hydrolysis of beef-heart cytochrome c. Oxidation-reduction potentials of the %%%heme%%% %%%peptide%%% in solutions containing imidazole were measured over the range of pH 4 to 13. The potentials observed differ greatly from the corresponding ones reported for cytochrome c, and resemble more nearly those found for horseradish peroxidase. The oxdiation-reduction potential of the imidazole-%%%heme%%% %%%peptide%%% system (ferri-ferro) at pH 7 and 30[degree] is -0.195 volt. The variation of potential with pH indicates oxidation-linked proton functions with the following pK[image] values: oxidized form, 6.6, 10.5, and 11.1; reduced form, 4.6, 5.6, 7.2, and 9.8. Conditions were determined under which various solutions of the %%%heme%%% %%%peptide%%% appear free of irreversible effects, and the variation with pH of the absorption spectra displayed under such conditions was examined for both the oxidized and reduced forms of the %%%heme%%% %%%peptide%%%. The relationship between the spectrophotometric observations and the oxidation-reduction data has been considered, and has formed a basis for discussion of the processes reflected in the experimental results reported. ABSTRACT AUTHORS: Auth. sum

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3/7/25
DIALOG(R)File 5:Biosis Previews(R)

12833765 BIOSIS NO.: 199598301598
Identification of a common epitope near the conserved %%%heme%%% %%%peptide%%% in several cytochrome P450 enzymes.
AUTHOR: Guengerich F P; Soucek P; Martin M V; Ueng Y F; Bell L C
AUTHOR ADDRESS: Dep. Biochem., Vanderbilt Univ., Nashville, TN 37232, USA** USA
JOURNAL: FASEB Journal 9 (6): pA1487 1995 1995
CONFERENCE/MEETING: Annual Meeting of the American Society for Biochemistry and Molecular Biology San Francisco, California, USA May 21-25, 1995; 19950521
ISSN: 0892-6638
DOCUMENT TYPE: Meeting; Meeting Abstract
RECORD TYPE: Citation
LANGUAGE: English

3/7/26
DIALOG(R)File 5:Biosis Previews(R)

12652765 BIOSIS NO.: 199598120598

Interaction of tryptophan residues of cytochrome P450scc with a highly specific fluorescence quencher, a substrate analogue, compared to acrylamide and iodide

AUTHOR: Lange Reinhard (Reprint); Anzenbacher Pavel; Muller Sylvaine; Maurin Luc; Balny Claude
AUTHOR ADDRESS: INSERM U 128, BP 5051, Route de Mende, Campus CNRS, F-34033 Montpellier, France**France

JOURNAL: European Journal of Biochemistry 226 (3): p963-970 1994 1994
ISSN: 0014-2956
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The cytochrome P450scc tryptophan fluorescence was studied by the use of the three quenchers acrylamide, 25-doxyl-27-nor-cholesterol (CNO) and potassium iodide (KI). All the nine tryptophan residues were accessible to acrylamide. Whereas a strong interacation (static quenching) between acrylamide and tryptophan in the active site had been found previously for cytochrome P450c21 (Narasinihulu, S. (1988) Biochemistry 27, 1147-1153), in the case of P450scc the temperature dependence of the slope of the linear Stem-Volmer plots indicated a dynamic quenching mechanism. This mechanism was confirmed by fluorescence lifetime measurements. Of the three observed lifetimes tau-1 = 3.1 +- 0.5 ns, tau-2 = 0.7 +- 0.25 ns and tau-3 = 20 +- 10 ps, tau-1 decreased noticeably as a function of the acrylamide concentration. CNO, a spin-labeled substrate which is known to bind tightly to the substrate-binding site of P450scc, quenched 15.5% of the total fluorescence. The Lehrer plot of this compound indicated a static quenching process with a reciprocal quenching constant of 1/K-s = 4 mu-M, a value which is in accord with the dissociation constant. Our data indicate that CNO quenches selectively one or two tryptophan residue(s) in the acive site. The fluorescence spectrum of the residue(s) accessible to CNO was characterized by a red-shifted emission maximum (from 332 nm to 336 nm). The same residue(s) appeared to be quenched by potassium iodide, although much less effectively (1/K-s = 0.12 M). The most probable candidate for a complex formation with CNO is Trp417, which is rather close to Cys422 (the fifth heme ligand). Four arginine residues (Arg411, Arg420, Arg425 and Arg426) in the %%%heme%%% %%%peptide%%% may constitute the iodide-binding site.

12336762 BIOSIS NO.: 199497358047

Moessbauer spectra of the %%%heme%%% %%%peptide%%% (HP) 1-50 and the %%%heme%%% %%%peptide%%%: Non-%%%heme%%% %%%peptide%%% (HNP) non-covalent complex 1-50:51-104 derived from cytochrome c: Evidence for cytochrome c iron site solvation in aqueous solution

AUTHOR: Adams Paul A; Milton Raymond C De L; Silver Jack (Reprint)
AUTHOR ADDRESS: Dep. Chem. Biol. Chem., Univ. Essex, Wivenhoe Park, Colchester CO4 3SQ, UK**UK

JOURNAL: Biometals 7 (3): p217-220 1994 1994
ISSN: 0966-0844
DOCUMENT TYPE: Article
RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Moessbauer spectroscopic studies on a %%%heme%%% %%%peptide%%% (HP) derived from cytochrome c and on the HP recombined non-covalently with the remaining cleaved section are reported. The results suggest that the environment of the heme site in the known crystal structure of cytochrome c may differ in detail from the environment of the heme in the working protein.

3/7/28
DIALOG(R)File 5:Biosis Previews(R)

12305498 BIOSIS NO.: 199497326783
%%%Haem%%% %%%peptide%%%/protein interaction part 6: The kinetic mechanisms of the interactions with, and inhibition of enzymic activity of the human erythrocyte glutathione S-transferase isoenzyme rho (p), by haem octa-, nona-, and undecapeptides MP-8/-9/-11
AUTHOR: Thumser A E A; Adams P A (Reprint)
AUTHOR ADDRESS: MRC Biomembrane Research Unit, Dep. Chem. Pathol., Univ. Cape Town Med. Sch., Observatory, 7925, Cape Town, South Africa**South Africa
JOURNAL: Journal of Inorganic Biochemistry 53 (3): p157-168 1994 1994
ISSN: 0162-0134
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The binding of the cytochrome-c derived haem peptides microperoxidase-8, -9, and -11 (MP-8, -9, and -11) to the human erythrocyte glutathione S-transferase rho (GST-p) enzyme is demonstrated. Inhibition by the haem peptides of the enzymic conjugation of glutathione (GSH) with the electrophilic cosubstrate 1-chloro-2,4-dinitrobenzene (CDNB) is mixed-type with respect to CDNB, and K-i, the inhibition constant, increases with increasing length of the peptide chain. The results obtained here for the GST-p are compared to those published recently for the previously supposed identical isoenzyme human placental GST-pi.

3/7/29
DIALOG(R)File 5:Biosis Previews(R)

11862848 BIOSIS NO.: 199396027264
Reduction of nitro and Azo compounds by NADPH cytochrome P-450 reductase-cytochrome c %%%heme%%% %%%peptide%%% system
AUTHOR: Masuda Yasusuke (Reprint); Ozaki Masanobu
AUTHOR ADDRESS: Div. Toxicology, Niigata Coll. Pharmacy, Niigata 950-21, Japan**Japan
JOURNAL: Biological and Pharmaceutical Bulletin 16 (2): p112-115 1993
ISSN: 0918-6158
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Octa %%%heme%%% %%%peptide%%%, an enzymic digestion product of Candida Krusei cytochrome c, was found to catalyze nitro and azo reduction in the presence of NADPH and NADPH-cytochrome P-450 reductase under anaerobic conditions. The reduction was dependent on the concentration of %%%heme%%% %%%peptide%%% and reductase, and inhibited by carbon monoxide and oxygen. Comparison of the activities of the reductase-%%%heme%%% %%%peptide%%% system with liver microsomes revealed that %%%heme%%% %%%peptide%%% was as effective as cytochrome P-450 in nitro reduction, although less effective in azo reduction. Thus, cytochrome c %%%heme%%% %%%peptide%%% may serve as an artificial substitute for cytochrome P-450 at least in the reductive metabolism of xenobiotics.

3/7/30
DIALOG(R)File 5:Biosis Previews(R)

11836199 BIOSIS NO.: 199396000615
%%%Haem%%%-%%%peptide%%%-protein interactions: Part 5. The haem undecapeptide microperoxidase-11 (Fe-3+MP-11)/human serum albumin (HSA) reaction in aqueous methanolic solution: A simple system demonstrating the effect of hydrophobicity on ligand release from a ligand-protein complex
AUTHOR: Adams Paul A (Reprint); Thumser Alfred E A
AUTHOR ADDRESS: MRC Biomembrane Res. Unit, Dep. Chemical Pathology, Univ. Cape Town Med. Sch., Observatory 7925, South Africa**South Africa
JOURNAL: Journal of Inorganic Biochemistry 50 (1): p1-7 1993
ISSN: 0162-0134
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Previous studies of the interaction of the haem undecapeptide (MP-11) with lipidated human serum albumin in aqueous solution have been extended to a range of MeOH/H-20 solution compositions. It is demonstrated that the kinetic mechanism for the interaction does not change from a simple second- and first-order reversible scheme as X-MeOH is increased, however while k-1 - the association rate constant is essentially invariant with X-MeOH, k-1 increases some 600-fold over the range studied. The result is interpreted in terms of increased solvational stabilization of MP-11 and transition state as X-MeOH increases and it is noted that the system provides a simple demonstration of the effect of hydrophobicity on facilitating transported ligand release from ligand/carrier protein molecules.

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DIALOG(R)File 5:Biosis Previews(R)

11732813 BIOSIS NO.: 199395035079
Adsorption of heme-containing peptides on silicon surfaces
AUTHOR: Ruzgas Tautgirdas A (Reprint); Kazlauskas Ausvydas V; Razumas Valdemaras J; Kulys Juozas J
AUTHOR ADDRESS: Dep. Enzyme Chem., Lithuanian Acad. Sci., Moksliniku 12, Vilnuis 2600, Lithuania**Lithuania

JOURNAL: Journal of Colloid and Interface Science 154 (1): p97-103 1992
ISSN: 0021-9797
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: To elucidate the role of minor alteration of amino acid composition of protein in interfacial behavior, the adsorption of three heme peptides on hydrophilic and hydrophobic silicon surfaces was studied. It was found that all three peptides did not adsorb on the hydrophilic silicon surfaces and irreversibly adsorbed on the hydrophobic silica prepared by pretreatment with dimethyldichlorosilane. Rate constants of adsorption at pH = 7.2 for all the heme peptides were the same, indicating that at the initial stage of adsorption heme peptides interacted with the hydrophobic surface through identical segments. On the basis of plateau values obtained, calculation of surface areas occupied per %%%heme%%% %%%peptide%%% molecule showed that the higher the %%%heme%%% %%%peptide%%% molecular mass, the smaller is its occupied area on the hydrophobic silicon surface at pH = 7.2. This "illogical" observation was explored by electrostatic interaction of adsorbed %%%heme%%% %%%peptide%%% molecules, on the basis of their a bell-shaped pH-dependent adsorption and on the pK-a values of amino acid residues in heme peptides.

11322732 BIOSIS NO.: 199294024573
BILAYER STRUCTURE AND PHYSICAL DYNAMICS OF THE CYTOCHROME B-5 DIMYRISTOYLPHOSPHATIDYLCHOLINE INTERACTION
AUTHOR: CHESTER D W (Reprint); SKITA V; YOUNG H S; MAVROMOUSTAKOS T; STRITTMATTER P
AUTHOR ADDRESS: BIOMOL STRUCTURE ANAL CENT, UNIV CONN HEALTH CENT, FARMINGTON, CONN 06030, USA**USA
JOURNAL: Biophysical Journal 61 (5): p1224-1243 1992
ISSN: 0006-3495
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Cytochrome b5 is a microsomal membrane protein which provides reducing potential to .DELTA.5-, .DELTA.6- and .DELTA.9-fatty acid desaturases through its interaction with cytochrome b5 reductase. Low angle x-ray diffraction has been used to determine the structure of an asymmetrically reconstituted cytochrome b5:DMPC model membrane system. Differential scanning calorimetry and fluorescence anisotropy studies were performed to examine the bilayer physical dynamics of this reconstituted system. These latter studies allow us to constrain structural models to those which are consistent with physical dynamics data. Additionally, because the nonpolar peptide secondary structure remains unclear, we tested the sensitivity of our model to different nonpolar peptide domain configurations. In this modeling approach, the nonpolar peptide moiety was arranged in the membrane to meet such chemically determined criteria as protease susceptibility of carboxyl- and amino-termini, tyrosine availability for pH titration and tryptophan

109 location, et cetera. In these studies, we have obtained a reconstituted cytochrome b5:DMPC bilayer structure at .apprx.6.3 .ANG. resolution and conclude that the nonpolar peptide does not penetrate beyond the bilayer midplane. Structural correlations with calorimetry, fluorescence anisotropy and acyl chain packing data suggest that asymmetric cytochrome b5 incorporation into the bilayer increases acyl chain order. Additionally, we suggest that the %%%heme%%% %%%peptide%%% :bilayer interaction facilitates a discrete %%%heme%%% %%%peptide%%% orientation which would be dependent upon phospholipid headgroup composition.

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DIALOG(R)File 5:Biosis Previews(R)

11229874 BIOSIS NO.: 199293072765
PEROXIDASE MODEL ELECTRODES SENSING OF IMIDAZOLE DERIVATIVES WITH %%%HEME%%% %%%PEPTIDE%%%-MODIFIED ELECTRODES
AUTHOR: TATSUMA T (Reprint); WATANABE T
AUTHOR ADDRESS: INSTITUT OF INDUSTRIAL SCI, UNIV TOKYO, ROPPONGI, MINATO-KU, TOKYO 106, JAPAN**JAPAN
JOURNAL: Analytical Chemistry 64 (2): p143-147 1992
ISSN: 0003-2700
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A tin(IV) oxide electrode covalently modified with heme nonapeptide, a peroxidase model, was examined as an interference-based amperometric sensor for imidazole derivatives. The current for catalytic H2O2 reduction on the %%%heme%%% %%%peptide%%% electrode is inhibited by compounds, either ionic or neutral, which coordinate strongly to the Fe(III) atom of the heme, and this phenomenon was utilized for their amperometric detection in the presence of H2O2. The response time was shorter than 10 s. The selectivity sequence was imidazole > 1-methylimidazole > 4-methylimidazole .gtoreq. histamine > histidine > SCN- > salicylate .gtoreq. I- .gtoreq. NO2- .gtoreq. ClO4- > 2-methylimidazole, Br-, Cl- methanol, and ethanol, where the last five species were completely silent. The inertness of 2-methylimidazole arises probably from a steric hindrance for ligation to Fe(III). The results of kinetic analysis of the interfacial processes are also presented.

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DIALOG(R)File 5:Biosis Previews(R)

11178830 BIOSIS NO.: 199293021721
%%%HEME%%% %%%PEPTIDE%%% AS A MODEL SUBSTANCE FOR HALOGENOMETHANE ACTIVATION AND HEME MODIFICATION
AUTHOR: MASUDA Y (Reprint); OIKAWA K; IMAIZUMI N; KATO A; MURANO T
AUTHOR ADDRESS: DIV TOXICOL, NIIGATA COLL PHARMACY, 5-13-2 KAMISHIN'EI-CHO, NIIGATA 950-21, JAPAN**JAPAN
JOURNAL: Biochimica et Biophysica Acta 1075 (2): p131-138 1991
ISSN: 0006-3002
DOCUMENT TYPE: Article

RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Octa-%%%heme%%% %%%peptide%%% (CHP) obtained from Candida krusei cytochrome c was tested for suicidal activation of halogenomethanes. Under anerobic conditions, CHP was kept in the reduced state in the presence of NADPH and NADPH-cytochrome P-450 reductase. Addition of CBrCl3 to the reduced CHP caused spectral changes such as rapid disappearance of .alpha. and .beta. bands and gradual decrease in the .gamma.-peak height, accompanied by oxidation of NADPH. Heme content of the reaction mixture, determined as pyridine hemochrome, also decreased NADPH dependently. CCl4 was less effective than CBrCl3, while CHCl3 had almost no effect. N-tert-butyl-.alpha.-phenylnitrone (PBN) suppressed the CBrCl3-induced heme damage, and resulted in the formation of radical adduct .cntdot.PBN-CCl3 as evidenced by ESR spectroscopy. Radical formation was also observed with CCl4. The CHP damage induced by CBrCl3 was also accompanied by the release of Br- about 11-12-times molar excess of CHP, whereas the release of CHCl3 was about 20% that of Br-. FD-MS assay of the product of CHP reaction suggested that 10 trichloromethyl radicals bonded with CHP. Thus, CBrCl3 undergoes single-electron reduction in the presence of reduced CHP to trichloromethyl radicals, which covalently bind to CHP molecules. %%%Heme%%% %%%peptide%%% may be a useful tool in the study of mechanisms involved in the destruction of cytochrome P-450 by halogenomethanes.

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10883239 BIOSIS NO.: 199192129010
SOLUTION STRUCTURE OF IRON-II CYTOCHROME C551 FROM PSEUDOMONAS-AERUGINOSA AS DETERMINED BY TWO-DIMENSIONAL PROTON NMR
AUTHOR: DETLEFSEN D J (Reprint); THANABAL V; PECORARO V L; WAGNER G
AUTHOR ADDRESS: DEP BIOLOGICAL CHEM, HARVARD MED SCH, 240 LONGWOOD AVE, BOSTON, MASS 02115, USA**USA
JOURNAL: Biochemistry 30 (37): p9040-9046 1991
ISSN: 0006-2960
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The solution structure of Fe(II) cytochrome c551 from Pseudomonas aeruginosa based on 2D 1H NMR data is reported. Two sets of structure calculations were completed with a combination of simulated annealing and distance geometry calculations: one set of 20 structures included the %%%heme%%%-%%%peptide%%% covalent linkages, and one set of 10 structures excluded them. The main-chain atoms were well constrained within the two structural ensembles (1.30 and 1.35 .ANG. average RMSD, respectively) except for two regions spanning residues 30-40 and 60-70. The results were essentially the same when global fold comparisons were made between the ensembles with an average RMSD of 1.33 .ANG.. In total, 556 contraints were used, including 479 NOEs, 53 volume constraints, and 24 other distances. This report represents the first solution structure determination of a heme protein by 2D 1H NMR and should provide a basis for the application of these techniques to other proteins containing large prosthetic groups or cofactors.

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DIALOG(R)File 5:Biosis Previews(R)

10837770 BIOSIS NO.: 199192083541
PEROXIDASE MODEL ELECTRODES %%%HEME%%% %%%PEPTIDE%%% MODIFIED ELECTRODES AS REAGENTLESS SENSORS FOR HYDROGEN PEROXIDE
AUTHOR: TATSUMA T (Reprint); WATANABE T
AUTHOR ADDRESS: INST INDUSTRIAL SCI, UNIV, TOKYO, ROPPONGI, MINATO-KU, TOKYO 106, JPN**JAPAN
JOURNAL: Analytical Chemistry 63 (15): p1580-1585 1991
ISSN: 0003-2700
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A peroxidase model electrode was devised for reagentless sensing of hydrogen peroxide (H2O2). A small model molecule, which mimics the vicinity of the reaction center of a redox enzyme, can communicate electrochemically with an electrode. Heme nonapeptide (MW .simeq. 1600) having peroxidase activity was adopted as a peroxidase model compound and was covalently immobilized on a tin oxide (SnO2) electrode as a roughly monomolecular layer. The modified electrode thus obtained responded to H2O2 at concentrations down to 10-6 M without electron mediator or promoter, at a mild potential of +150 or +300 mV as Ag/AgCl. In a batch system, the response reached a steady state in a few secods. Measurements were possible also in a flow system with an assay time of 0.5-1.0 min/samples. The steady-state response of the electrode was kinetically analyzed.

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DIALOG(R)File 5:Biosis Previews(R)

10768894 BIOSIS NO.: 199192014665
MECHANISM OF THE ANTIOXIDANT EFFECT OF CYTOCHROME C HEME NONAPEPTIDE
AUTHOR: LYSKO A I (Reprint); LUK'YANOVA L D; DUDCHENKOK A M; ARUTYUNYAN A M ; ZHURAVLEVA D V; KULISH M A; MIRONOV A F; EVSTIGNEEVA R P
AUTHOR ADDRESS: RES INST PHARMACOL, ACAD MED SCI USSR, MOSCOW, USSR**USSR
JOURNAL: Doklady Akademii Nauk SSSR 315 (2): p500-504 1990
ISSN: 0002-3264
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: RUSSIAN

ABSTRACT: The possibility of the existence of an alternative mechanism of the antioxidant activity of heme peptides was investigated. This activity is determined by the peroxidase properties of heme peptides when pyridine nucleotides are used as electron donors. Pyridine nucleotides play a central role in cell energy metabolism. The effect of the formation of %%%heme%%% %%%peptide%%% and cytochrome P-450 substrate complexes on the kinetics of peroxidase reaction was evaluated. Data were presented on NADP-H and O2 consumption during NADP-H-dependent lipid peroxidation in rat liver microsomes. It was confirmed that reduced pyridine nucleotides

can be used as electron donors in a peroxidase reaction catalyzed by heme nonapeptide. Apparently, this reaction is shifted in the direction of heterolytic mechanism in the presence of aniline and aminopyrine which form complexes with heme nonapeptide.

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DIALOG(R)File 5:Biosis Previews(R)

10316319 BIOSIS NO.: 199090100798
%%%HEME%%% %%%PEPTIDE%%%-PROTEIN INTERACTIONS PART 4. THE MICROPEROXIDASE-8-MEDIATED INHIBITION OF THE HUMAN PLACENTAL GLUTATHIONE S-TRANSFERASE PI CATALYSED CONJUGATION OF GLUTATHIONE AND 1 CHLORO-2 4-DINITROBENZENE
AUTHOR: ADAMS P A (Reprint); GOOLD R D
AUTHOR ADDRESS: MCR BIOMEMBRANE RES UNIT, DEP CHEM PATHOL, UNIV CAPE TOWN, MED SCH, OBSERVATORY 7925, CAPE PROVINCE, SOUTH AFRICA**SOUTH AFRICA
JOURNAL: Journal of the Chemical Society Faraday Transactions 86 (10): p 1803-1806 1990
ISSN: 0956-5000
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The inhibition of the glutathione S-transferase .pi. (GST) catalysed conjugation of glutathione (GSH) with 1-chloro-2,4-dinitrobenzene (CDNB) by the haem octapeptide microperoxidase-8 (MP-8) has been investigated. Incubation of the enzyme with MP-8 results in a pseudo-first-order partial inactivation of the enzyme [kobs = 2.3 (.+-.0.4) .times. 10-3 s-1; pH 6.5; 22.5.degree.C]. The kobs is identical to that found for dilutional inactivation of the enzyme observed in buffer alone. MP-8 increases only the extent of inactivation above that observed for dilutional inactivation. Incubation of the enzyme with varying concentrations of MP-8 was followed by a steady-state kinetic study of the enzyme-catalysed conjugation of GSH with CDNB at (a) fixed [GSH], varying [CDNB] and (b) fixed [CDNB] varying [GSH]. In case (a) the data conformed closely with mixed competitive/non-competitive inhibition kinetics (Ki = 3.2 .times. 10-7 mol dm-3, pH 6.5, 30 .degree.C), while in case (b) the extent of inhibition was insufficient to allow analysis. These observations are rationalized and discussed in the light of the kinetic studies of MP-8 binding to GST .pi. reported in the preceding paper.

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DIALOG(R)File 5:Biosis Previews(R)

10313681 BIOSIS NO.: 199090098160
%%%HEME%%% %%%PEPTIDE%%%-PROTEIN INTERACTIONS PART 3. THE KINETICS AND MECHANISM OF THE INTERACTION BETWEEN HUMAN PLACENTAL GLUTATHIONE S-TRANSFERASE PI AND THE NON-SUBSTRATE LIGAND MICROPEROXIDASE-8 MP-8
AUTHOR: ADAMS P A (Reprint); GOOLD R D
AUTHOR ADDRESS: MRC BIOMEMBRANE RES UNIT, DEP CHEM PATHOL, UNIV CAPE TOWN, MED SCH, OBSERVATORY 7925, CAPE PROVINCE, SOUTH AFRICA**SOUTH AFRICA
JOURNAL: Journal of the Chemical Society Faraday Transactions 86 (10): p

1797-1802 1990
ISSN: 0956-5000
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The kinetics of the reaction between the %%%haem%%%-%%%peptide%%% microperoxidase-8 and human placental glutathione S-transferase .pi. have been followed using the quenching of the MP-8 Soret absorbance, which is observed on mixing the two species. Under pseudo-first-order conditions ([MP-8] .mchgt. [GST]) and over a concentration range in which the MP-8 is monomeric in aqueous solution, the binding curves are biphasic. The rapid phase of binding is associated with a hydrophobic site at or close to the binding site for the co-substrate 1-chloro-2,4-dinitrobenzene (CDNB), while the slow-binding phase reflects hydrophobic interaction with or spatially close to the bilirubin binding site on the enzyme. The mechanism for the interaction has been shown to be of the random sequential form with perturbation due to solvational elimination of the fast site. These studies recommend MP-8 as a useful non-substrate ligand model for monomeric haemin with which to study the kinetics and mechanism of ligand binding to the glutathione S-transferases.

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DIALOG(R)File 5:Biosis Previews(R)

10139982 BIOSIS NO.: 199089057873
%%%HEME%%% %%%PEPTIDE%%%-PROTEIN INTERACTIONS PART 2. KINETICS AND MECHANISM OF THE INTERACTION OF MICROPEROXIDASE-8 WITH APOMYOGLOBIN
AUTHOR: ADAMS P A (Reprint); GOOLD R D; THUMSER A E
AUTHOR ADDRESS: DEP CHEM PATHOL, UNIV CAPE TOWN, MED SCH, OBSERVATORY 7925, S AFR**SOUTH AFRICA
JOURNAL: Journal of the Chemical Society Faraday Transactions I 85 (11): p 3845-3852 1989
ISSN: 0300-9599
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The kinetics of the interaction between the haem octapeptide microperoxidase-8 (MP-8) and apomyoglobin (apoMb) have been investigated as a model for the reaction of monomeric ferriproporphyrin IX (haemin) with apohaemoproteins. The kinetics of the reaction are consistent with a two-stage single-intermediate interaction process. Close agreement between the association constant calculated using microscopic rate constants, and that measured by spectrophotometric titration provides powerful positive evidence for the correctness of the proposed mechanism. On the basis of the kinetic binding studies and spectrophotometric observation of the reduction of the Fe3-MP-8 apoMb complex we propose a novel equilibrium between a bis- and mono-axially histidyl ligated iron species for the peptide-protein complex in solution.

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DIALOG(R)File 5:Biosis Previews(R)

10093461 BIOSIS NO.: 199089011352
%%%HEME%%%-%%%PEPTIDE%%%-PROTEIN INTERACTIONS THE BINDING OF HEME OCTA AND UNDECAPEPTIDES AND MICROPEROXIDASE-8 AND 11 TO HUMAN SERUM ALBUMIN
AUTHOR: ADAMS P A (Reprint); GOOLD R D; THUMSER A A
AUTHOR ADDRESS: DEP CHEMICAL PATHOLOGY, MED SCH OBSERVATORY 7925, CAPE TOWN, SOUTH AFRICA**SOUTH AFRICA
JOURNAL: Journal of Inorganic Biochemistry 37 (2): p91-104 1989
ISSN: 0162-0134
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The interaction of the heme octa (MP-8) and undeca (MP-11) peptides derived from cytochrome c with lipidated human serum albumin (HSA) has been investigated in aqueous solution. It is demonstrated that complex formation occurs in each case with a 1:1 stoichiometry. CN- binding has been used to investigate the accessibility of the heme in each complex by comparison with CN- interaction with methemalbumin. A preliminary study of the kinetics of the Fe3+ MP-8/11 human serumalbumin (HSA) interaction demonstrates a clear ligand-size-related effect on mechanism of interaction-an ad hoc explanation of which is given in terms of HSA existing as two nonconverting conformers in solution.

09736184 BIOSIS NO.: 198988051299
REACTIONS OF THE PROTEIN RADICAL IN PEROXIDE-TREATED MYOGLOBIN FORMATION OF A HEME-PROTEIN CROSS-LINK
AUTHOR: CATALANO C E (Reprint); CHOE Y S; ORTIZ DE MONTELLANO P R
AUTHOR ADDRESS: DEP PHARMACEUTICAL CHEM, SCH PHARMACY AND LIVER CENT, UNIV CALIFORNIA, SAN FRANCISCO, CALIF 94143, USA**USA
JOURNAL: Journal of Biological Chemistry 264 (18): p10534-10541 1989
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Reaction of horse myoglobin with H2O2 oxidizes the iron to the ferryl (Fe(IV)=O) state and produces a protein radical that is rapidly dissipated by poorly understood mechansisms. As reportecd here, the reaction with H2O2 results in covalent binding of up to 18% of the prosthetic heme group to the protein. The chromophore of the protein-bound prosthetic group is very similar to that of heme itself. High performance liquid chromatography of tryptic digests indicates that the formation of heme-bound peptides is associated with disappearance of the peptide with the sequence YLE-FISDAIIHVLHSK corresponding to residues 103-118 of horse myoglobin. Amino acid analysis, terminal amino acid sequencing, and liquid secondary ion mass spectrometry establish that the heme is primarily attached to this peptide. The heme appears to be bound to the tyrosine residue because the tyrosine is the only amino acid that disappears from the amino acid analysis. The mass spectrometric data indicates that the %%%heme%%%-%%%peptide%%% is formed without addition or loss of an oxygen or other major structural fragment. The site of

attachment to the heme group has not been unambiguously determined, but the heme vinyl groups are not essential for the reaction because equal cross-linking is observed in H2O2-treated mesoheme-reconstituted myoglobin. The results are most consistent with binding of tyrosine 103 to a meso-carbon of the prosthetic heme group.

3/7/43
DIALOG(R)File 5:Biosis Previews(R)

09356771 BIOSIS NO.: 198936065662
HYDROXYLATION OF ANILINE MEDIATED BY HEME-BOUND OXY-RADICALS IN A %%%HEME%%% %%%PEPTIDE%%% MODEL SYSTEM
AUTHOR: RUSVAI E (Reprint); VEGH M; KRAMER M; HORVATH I
AUTHOR ADDRESS: SECOND INST BIOCHEM, SEMMELWEISS UNIV MED SCH, 1444 BUDAPEST PF262, HUNGARY**HUNGARY
JOURNAL: Biochemical Pharmacology 37 (23): p4574-4577 1988
ISSN: 0006-2952
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: ENGLISH

3/7/44
DIALOG(R)File 5:Biosis Previews(R)

09173386 BIOSIS NO.: 198886013307
CHICKEN LIVER SULFITE OXIDASE KINETICS OF REDUCTION BY LASER-PHOTOREDUCED FLAVINS AND INTRAMOLECULAR ELECTRON TRANSFER
AUTHOR: KIPKE C A (Reprint); CUSANOVICH M A; TOLLIN G; SUNDE R A; ENEMARK J E
AUTHOR ADDRESS: DEP BIOCHEM, UNIV ARIZ, TUCSON, ARIZ 85721, USA**USA
JOURNAL: Biochemistry 27 (8): p2918-2926 1988
ISSN: 0006-2960
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Laser flash photolysis was used to study the reaction of photoproduced 5-deazariboflavin (dRFH .cntdot.), lumiflavin (LFH .cntdot.), and riboflavavin (RFH .cntdot.) semiquinone radicals with the redox centers of purified chicken liver sulfite oxidase. Kinetic studies of the native enzyme with dRFH .cntdot. yielded a second-order rate constant of 4.0 .times. 108 M-1 s-1 for direct reduction of the heme and a first-order rate constant of 310 s-1 for intramolecular electron transfer from the Mo center to the heme. The reaction with LFH .cntdot. gave a second-order rate constant of 2.9 .times. 107 M-1 s-1 for heme reduction. Reoxidation of the reduced of the reduced heme due to intramolecular electron transfer to the Mo center gave a first-order rate constant of 155 s-1. The direction of intramolecular electron transfer using dRFH .cntdot. and LFH .cntdot. was independent of the buffer used for the experiment. The different first-order rate constants observed for intramolecular electron transfer using dRFH .cntdot. and LFH .cntdot. are proposed to result from chemical differences at the Mo site. Flash photolysis studies with cyanide-inactivated sulfite oxidase using dRFH

.cntdot. and LFH .cntdot. resulted in second-order reduction of the heme center with rate constants identical with those obtainedwith the native enzyme, whereas the first-order intramolecular electron-transfer processes seen with the native enzyme were absent. The isolated %%%heme%%% %%%peptide%%% of sulfite oxidase gave only second-order kinetics upon laser photolysis and confirmed that the first-order processes observed with the native enzyme involve in the Mo site. The flash-induced difference spectrum of native sulfite oxidase using dRFH .cntdot. and LFH .cntdot. resulted in absorbance increases in the 530-570-nm region of the spectrum that were not present in the static difference spectrum of the enzyme. These absorbances and proposed to be associated with the Mo center.

3/7/45
DIALOG(R)File 5:Biosis Previews(R)

09085453 BIOSIS NO.: 198885054344
INTERACTION OF HEME WITH A SYNTHETIC PEPTIDE MIMICKING THE PUTATIVE HEME-BINDING SITE OF HISTIDINE-RICH GLYCOPROTEIN
AUTHOR: KATAGIRI M (Reprint); TSUTSUI K; YAMANO T; SHIMONISHI Y; ISHIBASHI F
AUTHOR ADDRESS: DEP CHEM, OSAKA KYOIKU UNIV, TENNOJI-KU, OSAKA 543, JPN** JAPAN
JOURNAL: Biochemical and Biophysical Research Communications 149 (3): p 1070-1076 1987
ISSN: 0006-291X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We synthesized a hexapeptide, Gly-His-His-Pro-His-Gly, previously identified as a tandem motif in the histidine-rich glycoprotein (HRG) which has multiple heme-binding sites. Binding of heme to the peptide was demonstrated by the characteristic difference spectrum showing a close resemblance to that of HRG, implying that the peptide binds heme through biaxial coordination with histidine imidazoles. Furthermore, the EPR spectra of the %%%heme%%%-%%%peptide%%% and heme-HRG complexes were almost completley identical in pattern, showing signals characteristic of the low spin iron. The results suggest that the synthetic peptide simulates the heme-binding properties of HRG and that each tandem motif in HRG serves as a unitary binding site for heme.

3/7/46
DIALOG(R)File 5:Biosis Previews(R)

09085223 BIOSIS NO.: 198885054114
DETECTION OF PICOMOLE LEVELS IN LIPID HYDROPEROXIDES BY A CHEMILUMINESCENCE ASSAY
AUTHOR: MIYAZAWA T (Reprint); FUJIMOTO K; KANEDA T
AUTHOR ADDRESS: DEP FOOD CHEM, TOHOKU UNIV, TSUTSUMIDORI AMAMIYAMACHI 1-1, SENDAI 980, JAPAN**JAPAN
JOURNAL: Agricultural and Biological Chemistry 51 (9): p2569-2574 1987
ISSN: 0002-1369

DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A highly sensitive and simple chemiluminescent method for the quantitation of lipid hydroperoxides at the picomole level is described. The method is based on detecting the chemiluminescence generated during the oxidation of luminol by the reaction with hydroperoxide and cytochrome c under mild conditions. A semilogarithmic relationship was observed between the hydroperoxide added and the chemiluminescence produced. For lipid hydroperoxides, cytochrome c was the most favorable catalyst for generating the chemiluminescence, rather than cytochrome c %%%heme%%% %%%peptide%%% and horseradish peroxidase. This method had high sensitivity to methyl linoleate hydroperoxide, arachidonic acid hydroperoxide and cholesterol hydroperoxide, but low to t-butyl hydroperoxide, t-butyl perbenzoate, diacyl peroxides (lauroyl peroxode and benzoyl peroxide) and dialkyl peroxides (di-t-butyl peroxide and dicumyl peroxide).

3/7/47
DIALOG(R)File 5:Biosis Previews(R)

08579295 BIOSIS NO.: 198783058186
EFFECT OF A %%%HEME%%%-%%%PEPTIDE%%% DERIVED FROM CYTOCHROME-C ON LIPID PEROXIDATION I. EFFECTS ON BRAIN MICROSOMES
AUTHOR: VODNYANSZKY L (Reprint); MARTON A; VEGH M; BLAZOVITS A; AUTH F; VERTES A; HORVATH I
AUTHOR ADDRESS: SECOND INST OF BIOCHEMISTRY, SEMMELWEIS UNIV MED SCH, BUDAPEST, HUNGARY**HUNGARY
JOURNAL: Acta Biochimica et Biophysica Hungarica 21 (1-2): p3-12 1986
ISSN: 0237-6261
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Heme-nonapeptide inhibits NADH and NADPH dependent lipid peroxidation of brain microsomes in the presence or absence of ADP-Fe complex. The transient accumulation of lipid peroxides during NADH or NADPH dependent, ADP-Fe stimulated lipid peroxidation, is inhibited by heme-nonapeptide. Oxygen consumption of brain microsomes in the presence of NADH and NADPH is stimulated by heme-nonapeptide. Reduction of cytochrome-c and nitro-tetrazolium-blue by O2 generated by xanthine oxidase is inhibited by heme-nonapeptide.

3/7/48
DIALOG(R)File 5:Biosis Previews(R)

08578888 BIOSIS NO.: 198783057779
EFFECT OF A %%%HEME%%%-%%%PEPTIDE%%% DERIVED FROM CYTOCHROME-C ON LIPID PEROXIDATION II. EXPERIMENTS WITH LIVER MICROSOMES
AUTHOR: VENEKEI I (Reprint); KNITTEL A; HORVATH I
AUTHOR ADDRESS: SECOND INST OF BIOCHEMISTRY, SEMMELWEIS UNIV MED SCH, BUDAPEST, HUNGARY**HUNGARY

JOURNAL: Acta Biochimica et Biophysica Hungarica 21 (1-2): p13-22 1986
ISSN: 0237-6261
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: ADP-Fe2+ stimulated, NADPH dependent lipid peroxidation of liver microsomes (as measured by malondialdehyde formation) was not inhibited by c-heme-nonapeptide, unlike the same process in brain microsomes. However, in the presence of 5 mM aminopyrine (causing partial inhibition) or SKF-525A (a specific inhibitor of cytochrome P450) the residual activity of lipid peroxidation of liver microsomes was markedly inhibited by c-heme-nonapeptide. Further, c-heme-nonapeptide itself prevented the transient accumulation of lipid hydroperoxides during ADP-Fe2+ stimulated lipid peroxidation. These results led us to suggest two different pathways of lipid peroxidation. The first route involves cytochrome P450. The second pathway, which can be inhibited by c-heme-nonapeptide, appears to be more important physiologically.

3/7/49

08535619 BIOSIS NO.: 198783014510
TERMINATIONS OF PHOTORECEPTOR AXONS FROM DIFFERENT REGIONS OF THE COMPOUND EYE OF THE DESERT ANT CATAGLYPHIS-BICOLOR
AUTHOR: MEYER E P (Reprint); NASSEL D R
AUTHOR ADDRESS: DEP ZOOL, UNIV ZURICH, WINTERTHURERSTR 190, CH-8057 ZURICH, SWITZ**SWITZERLAND
JOURNAL: Proceedings of the Royal Society of London Series B Biological Sciences 228 (1250): p59-70 1986
ISSN: 0080-4649
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The morphology of the photoreceptors from different regions of the desert ant's compound eye is investigated by Golgi-impregnations and anterograde or retrograde %%%heme%%% %%%peptide%%% filling, combined with electron microscopy. A new type of receptor axon is described. This receptor is of the short (SVF) type but terminates in the proximal layer of the lamina (EPL-C), in contrast to the other short visual fibres, which terminate in the distal layer (EPL-A): Golgi-EM investigations show that this receptor axon belongs to the small photoreceptor R9. The receptor R9 appears to be pre- and postsynaptic to other receptor axons and to second order neurons. In each ommatidium, the axons of the two long photoreceptors (LVF) R1 and R5 (probably UV-receptors) remain paired down to their terminations in the distal layers of the medulla. The regional specialization of the retina (dorsal rim area (DRA), dorsal retina (DR) and ventral retina (VR)) is reflected by the morphology of the receptor terminals and the second order neurons. The lamina underlying the DRA consists of only one layer, an extended EPL-A; in the remainder of the eye, the lamina is trilayered. In the DRA all short visual fibres (SVF) are equal in length. The extension of the monopolar cell dendrites is restricted to one cartridge only. In the medulla, the terminals of the LVFS deriving from the DRA (R1 and R5) have more

extensive arborizations than elsewhere in the eye.

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3/7/1
DIALOG(R)File 5:Biosis Previews(R)

19382379 BIOSIS NO.: 200700042120
%%%Heme%%%-%%%peptide%%%/protein ions and phosphorous ligands: search for site-specific addition reactions
AUTHOR: Crestoni Maria Elisa (Reprint); Fornarini Simonetta
AUTHOR ADDRESS: Univ Roma La Sapienza, Dipartimento Studi Chim and Tecnol Sostanze Biologi, Piazzale Aldo Moro 5, I-00185 Rome, Italy**Italy
AUTHOR E-MAIL ADDRESS: mariaelisa.crestoni@uniroma1.it
JOURNAL: JBIC Journal of Biological Inorganic Chemistry 12 (1): p22-35 JAN 2007 2007
ISSN: 0949-8257
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: High-resolution Fourier transform ion cyclotron resonance mass spectrometry is employed to gain thorough kinetics and thermodynamics information on the reaction of free and ligated heme-type ions with selected ligands, with the aim of obtaining an insight into the coordination environment of the prosthetic group in a variety of biomolecular ions. Adopting a stepwise approach towards systems of increasing complexity, we examined the reactivity of free gaseous iron(III) protoporphyrin IX ions, Fe(III)-heme(+), of the charged species from microperoxidase-11 (MP11) (covalently peptide bound heme), and of the multiply charged ions from heme proteins, namely, cytochrome c (cyt c) and myoglobin (examples of noncovalently protein bound hemes). Among an array of test compounds allowed to react with Fe(III)-heme(+), OP(OMe)(3) and P(OMe)(3) proved to be similarly efficient ligands in the first addition step, yet displayed markedly distinct reactivity towards heme iron already engaged in axial coordination. The ease with which P(OMe)(3) acts as a second axial ligand is exploited to probe structural and conformational features of biomolecular ions. In this way, circumstantial evidence is gained of a folded conformation of +2 charge state ions from MP11 and an elongated one for the +3 charge state ions. Similarly, both the general reaction pattern and detailed kinetics and thermodynamics data point to a regiospecific addition reaction of P(OMe)(3) directed at the heme iron within multiply charged ions from cyt c. This unprecedented example of ion-molecule reaction which specifically involves a prosthetic group belonging to protein ions stands in contrast to the multiple, nonspecific interactions established by OP(OMe)(3) molecules with the protonated sites of multiply charged cyt c and apomyoglobin ions. This finding may develop and provide sensitive probes of the structure and bonding features of protein ions in the gas phase.

3/7/2
DIALOG(R)File 5:Biosis Previews(R)

18850145 BIOSIS NO.: 200600195540
A size dependent folding contour for cytochrome C
AUTHOR: Roy Shibsekhar; Singha Santiswarup; Bhattacharya Jaydeep; GhoshMoulick Ranjita; Dasgupta Anjan Kr (Reprint)
AUTHOR ADDRESS: Univ Calcutta, Dept Biochem, Calcutta 700019, W Bengal, India**India
AUTHOR E-MAIL ADDRESS: adbioc@caluniv.ac.in
JOURNAL: Biophysical Chemistry 119 (1): p14-22 JAN 1 2006 2006
ISSN: 0301-4622
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The paper describes an experimental construct of the folding route of the heme protein cytochrome-C. The construct highlights a slowing down near the nose of the folding funnel caused by the multiplicity of the energy traps near the native conformation created as a result of complex %%%heme%%%-%%%peptide%%% interaction. Interestingly the hydrodynamic size, the size heterogeneity and peroxidase activity serve as a triple measure of the distance of this near equilibrium departure from native conformation. Accordingly, the folding process is marked with a gradual and reversible reduction of mean hydrodynamic size, size heterogeneity and peroxidase activity (higher in unfolded state). The Dynamic Light Scattering based straightforward illustration of hydrodynamic size variation may serve as a model to slow folding observed in case of heme proteins, the heme itself serving as a natural facilitator for the native peptide conformation.

3/7/3

18471933 BIOSIS NO.: 200510166433
Iron absorption from concentrated hemoglobin hydrolysate by rat
AUTHOR: Vaghefi Nikta; Nedjaoum Fuzia; Guillochon Didier; Bureau Francois; Arhan Pierre; Bougle Dominique (Reprint)
AUTHOR ADDRESS: CHU Caen, Lab Physiol Digest and Nutritionnelle, F-14033 Caen, France**France
AUTHOR E-MAIL ADDRESS: bougle-d@chu-caen.fr
JOURNAL: Journal of Nutritional Biochemistry 16 (6): p347-352 JUN 2005 2005
ISSN: 0955-2863
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Although heme iron is highly bioavailable, the low iron content of hemoglobin prevents its use for dietary fortification; on the other hand, purified heme has low solubility and absorption rate. The present study was designed to assess the interactions between concentrated heme iron and peptides released during globin hydrolysis and cysteine and their relation with iron absorption.Hemoglobin was hydrolyzed by pepsin or subtilisin, and then, heme iron was concentrated by ultrafiltration. Iron absorption was studied in a Ussing chamber; gluconate was used as control. Iron uptake from nonconcentrated pepsin hydrolysate and

gluconate was lower than from other groups. Cysteine significantly enhanced iron uptake except from the concentrated subtilisin hydrolysate. There was no significant difference between cysteine-supplemented groups.According to the different hydrolysis pathways of enzymes, it is assumed that the presence of hydrophobic peptides and the strength of %%%heme%%%-%%%peptide%%% interactions are both determining factors of heme iron absorption. These interactions occur mainly before iron uptake, as emphasized by the effect of cysteine.

3/7/4
DIALOG(R)File 5:Biosis Previews(R)

18307070 BIOSIS NO.: 200510001570
Control of %%%heme%%% %%%peptide%%% activity by using phase transition polymers modified with inhibitors
AUTHOR: Komori Kikuo; Matsui Hitomi; Tatsuma Tetsu (Reprint)
AUTHOR ADDRESS: Univ Tokyo, Inst Ind Sci, Meguro Ku, Tokyo 1538505, Japan** Japan
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JOURNAL: Bioelectrochemistry 65 (2): p129-134 FEB 05 2005
ISSN: 1567-5394
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Catalytic activity of a %%%heme%%% %%%peptide%%% (HP) modified-electrode for H2O2 reduction was controlled by use of poly(N-isopropylacrylamide) modified with an inhibitory moiety, imidazole group. The polymers inhibited the catalytic activity below their lower critical solution temperature (LCST) where the polymers were dissolved and did not inhibit the activity above the LCST where the polymers were precipitated. A polymer with a longer side chain connecting with the imidazole group was more inhibitory than a polymer with a shorter side chain at temperatures below the LCST. Formation constants of dissolved HP-imidazole complexes were evaluated by spectroscopic means, and it was found that the polymers were more inhibitory than the corresponding monomers.

3/7/5
DIALOG(R)File 5:Biosis Previews(R)

18291861 BIOSIS NO.: 200500198926
Characterization of a novel microperoxidase from Marinobacter hydrocarbonoclasticus by electrospray ionization tandem mass spectrometry
AUTHOR: Di Tullio Alessandra; Caputi Lorenzo; Malatesta Francesco; Reale Samantha; De Angelis Francesco (Reprint)
AUTHOR ADDRESS: Dept Chem Chem Engn and Mat, Univ Aquila, Via Vetoio Coppito 2, I-67010, Coppito, Italy**Italy
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JOURNAL: Journal of Mass Spectrometry 40 (3): p325-330 March 2005 2005
MEDIUM: print
ISSN: 1076-5174 _(ISSN print)

DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Microperoxidases are. small heme-peptides obtained by proteolytic digestion of cytochrome c, exhibiting peroxidase activity. They consist of a short- or medium-length polypeptide chain, covalently linked to an iron protoporphyrin IX moiety via two thioether bonds involving Cys residues at the c-porphyrin A and B pyrrole rings. These small molecules are interesting for a wide range of possible applications. We have structurally characterized, by means of electrospray ionization (ESI) mass and tandem mass spectrometric experiments, a novel microperoxidase called MMP-5 (Marinobacter MicroPeroxidase-5), obtained by proteolytic digestion of cytochrome c552, a monoheminic electron-transfer protein isolated from Marinobacter hydrocarbonoclasticus. This microperoxidase, which still maintains the functional peptide moieties for peroxidase activity, is devoid of the two amino acids intercalating the Cys residues linked to the c-porphyrin, thus increasing its water solubility. Once submitted to the ESI source potential, MMP-5 showed an interesting tendency for the reduction of the iron protoporphyrin substructure. This behaviour was clearly evidenced by the mass shift exhibited by the reduced form. Copyright Copyright 2005 John Wiley & Sons, Ltd.

3/7/6
DIALOG(R)File 5:Biosis Previews(R)

18263926 BIOSIS NO.: 200500170662
Oxygen-binding heme complexes of peptides designed to mimic the heme environment of myoglobin and hemoglobin
AUTHOR: Atassi M Zouhair (Reprint); Childress Catherine
AUTHOR ADDRESS: Dept Biochem and Mol Biol, Baylor Coll Med, Houston, TX, 77030, USA**USA
AUTHOR E-MAIL ADDRESS: matassi@bcm.tmc.edu
JOURNAL: Protein Journal 24 (1): p37-49 January 2005 2005
MEDIUM: print
ISSN: 1572-3887 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Development of effective resuscitation agents for blood-loss replacement in trauma or surgery is extremely important despite substantial improvements in screening methods of blood from human donors. This paper reports the design and synthesis of peptides that mimic the natural environment of the heme group in myoglobin (Mb) and in the alpha- and beta-subunits of human adult hemoglobin (Hb). The designs were based on the fact that the heme group in the aforementioned proteins is sandwiched between helices E and F. Fifteen test peptides and six control peptides were synthesized, and their ability to form stable complexes with heme was investigated. It was found that none of the control peptides or proteins was able to bind heme. However, each of the peptides that were designed to mimic the E-F helices, and even shorter designs, which removed from this region residues that do not contribute to contacts with the heme group, were each able to bind one mole of heme per mole of peptide forming peptide-heme complexes that were stable to

manipulation and behaved as single molecular species. Oxygen binding measurements on the reduced peptide-heme complexes showed that these compounds bind oxygen and give visible spectra that were typical of oxygenated heme-proteins. In oxygen binding measurements done under different partial pressures of oxygen, the %%%heme%%%-%%%peptide%%% complexes gave hyperbolic oxygen-saturation curves, but showed slight differences in their P50 values. The P50 values ranged from 3.8 mmHg for the %%%heme%%%-%%%peptide%%% B7 complex to 13.7 mmHg for the %%%heme%%%-%%%peptide%%% D13 complex (under the same conditions, P50 values for Hb and Mb were 34.0 and 5.5 mmHg, respectively). It is concluded that peptide constructs designed to mimic the heme-binding regions of Mb or the Hb subunits were able to form coordinate 1:1 complexes with heme, and these complexes bind oxygen in a manner expected for single subunit heme proteins.

3/7/7
DIALOG(R)File 5:Biosis Previews(R)

18066153 BIOSIS NO.: 200400446942
Biosynthesis of artificial microperoxidases by exploiting the secretion and cytochrome c maturation apparatuses of Escherichia coli
AUTHOR: Braun Martin; Thony-Meyer Linda (Reprint)
AUTHOR ADDRESS: Inst Mikrobiol, ETH, Wolfgang Pauli Str 10, CH-8093, Zurich, Switzerland**Switzerland
AUTHOR E-MAIL ADDRESS: lthoeny@micro.biol.ethz.ch
JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 101 (35): p12830-12835 August 31, 2004 2004
MEDIUM: print
ISSN: 0027-8424 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Microperoxidases were initially isolated as peptide fragments containing covalently bound heme and are derived from naturally occurring c-type cytochromes. They are not only used as model compounds but also have potential applications as biosensors, electron carriers, photoreceptors, microzymes, and drugs. In a systematic attempt to define the minimal requirements for covalent attachment of hemes to c-type cytochromes, we have succeeded to produce artificial microperoxidases with peptide sequences that do not occur naturally and can be manipulated. The in vivo production of these microperoxidases requires targeting of the peptide to the bacterial periplasm, proteolytic processing of the signal peptide, and covalent attachment of heme to the signature motif CXXCIH by the cytochrome c maturation proteins CcmA-H. The peptides that bind heme carry a C-terminal histidine tag, presumably to stabilize the %%%heme%%% %%%peptide%%%. We present a heme cassette that is the basis for the de novo design of functional hemoproteins.

3/7/8
DIALOG(R)File 5:Biosis Previews(R)

17776248 BIOSIS NO.: 200400157005

A possible role for the covalent heme-protein linkage in cytochrome c revealed via comparison of N-acetylmicroperoxidase-8 and a synthetic, monohistidine-coordinated %%%heme%%% %%%peptide%%%.
AUTHOR: Cowley Aaron B; Lukat-Rodgers Gudrun S; Rodgers Kenton R; Benson David R (Reprint)
AUTHOR ADDRESS: Department of Chemistry, University of Kansas, Lawrence, KS, 66045, USA**USA
AUTHOR E-MAIL ADDRESS: drb@ku.edu
JOURNAL: Biochemistry 43 (6): p1656-1666 February 17, 2004 2004
MEDIUM: print
ISSN: 0006-2960 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: N-Acetylmicroperoxidase-8 (1) contains heme and residues 14-21 of horse mitochondrial cytochrome c (cyt c). The two thioether bonds linking protein to heme in cyt c are present in 1, and the native axial ligand His-18 remains coordinated to iron. As an approach to probing structural or functional roles played by the double covalent heme-protein linkage in cyt c, we have initiated a study in which the properties of 1 are compared with those of a synthetic mono-His coordinated %%%heme%%% %%%peptide%%% containing a single covalent linkage (2). One consequence of the greater conformational restriction imposed on peptide conformation in 1 is that His-Fe(III) coordination is apprx1.4 kcal/mol more favorable in 1 than in 2. This highlights a clear advantage conferred to cyt c by having two covalent heme-protein linkages rather than one: greater thermodynamic stability of the protein fold. EPR (11 K) and resonance Raman (298 K) studies reveal that 1 and 2 exhibit a thermal high-spin/low-spin ferric equilibrium but that low-spin character is considerably more pronounced in 1. In addition, the thioether 2-(methylthio)ethanol (MTE) coordinates 0.5 kcal/mol more strongly to 1 than to 2 in 60:40 H2O/CH3OH and only triggers the expected conversion of iron to the low-spin state characteristic of ferric cyt c in the case of 1. This demonstrates that the axial ligand field provided by an imidazole and a thioether is too weak to induce a high-spin to low-spin conversion in a ferric porphyrin. Our results suggest that a conformationally constrained double covalent heme-protein linkage, as exists in 1 and its parent protein cyt c, is an effective solution that nature has evolved to circumvent this limitation. We propose that the stronger His-Fe(III) coordination enabled by such a linkage serves to markedly enhance the effective ligand field strength of His-18. Our studies with 1 and 2 suggest that a double covalent linkage in cyt c may also enable energetically more favorable trans ligation of Met-80 than would be possible if only a single linkage were present. This would serve to further increase the stability of the protein fold and perhaps to increase the effective ligand field strength of Met-80 as well.

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17523192 BIOSIS NO.: 200300477147
Hydrogen peroxide biosensor based on microperoxidase-11 entrapped in lipid membrane.
AUTHOR: Huang Weimin; Jia Jianbo; Zhang Zheling; Han Xiaojun; Tang Jilin;

Wang Jianguo; Dong Shaojun; Wang Erkang (Reprint)
AUTHOR ADDRESS: State Key Laboratory of Electroanalytical Chemistry, Changchun Institute of Applied Chemistry, Chinese Academy of Sciences, Changchun, Jilin, 130022, China**China
AUTHOR E-MAIL ADDRESS: ekwang@ns.ciac.jl.cn
JOURNAL: Biosensors and Bioelectronics 18 (10): p1225-1230 September 2003 2003
MEDIUM: print
ISSN: 0956-5663
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A highly catalytic activity microperoxidase-11 (MP-11) biosensor for H2O2 was developed to immobilizing the %%%heme%%% %%%peptide%%% in didodecyldimethylammonium bromide (DDAB) lipid membrane. The enzyme electrode thus obtained responded to H2O2 without electron mediator or promoter, at a potential of +0.10 V versus AgAgCl. A linear calibration curve is obtained over the range from 2.0X10-5 to 2.4X10-3 M. The biosensor responds to hydrogen peroxide in 15 s and has a detection limit of 8X10-7 M (S/N=3) Providing a natural environment with lipid membrane for protein immobilization and maintenance of protein functions is a suitable option for the design of biosensors.

3/7/10
DIALOG(R)File 5:Biosis Previews(R)

16809006 BIOSIS NO.: 200200402517
Process development for heme-enriched peptide by enzymatic hydrolysis of hemoglobin
AUTHOR: In Man-Jin; Chae Hee Jeong; Oh Nam-Soon (Reprint)
AUTHOR ADDRESS: Department of Food Science and Technology, Kongju National University, 527, Yesan, Chungnam, 340-800, South Korea**South Korea
JOURNAL: Bioresource Technology 84 (1): p63-68 August, 2002 2002
MEDIUM: print
ISSN: 0960-8524
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: An efficient production method of heme-iron-enriched peptide was developed based on enzymatic hydrolysis. Hemoglobin hydrolysis, carried out stepwise with commercially available exopeptidase and endopeptidase, resulted in an increased degree of hydrolysis (DH). Exopeptidase-catalyzed protein hydrolysis formed low molecular weight peptides and amino acids. Different process parameters including dialysis and ultra- and diafiltration were evaluated. %%%Heme%%%/%%%peptide%%% ratio increased as molecular weight cut-off (MWCO) of the dialysis membrane increased. When the hydrolysate was dialyzed against sodium phosphate buffer, a higher %%%heme%%%/%%%peptide%%% ratio was obtained. The %%%heme%%%/%%%peptide%%% ratio of the hydrolysate reached up to 25.4% when the dialysis was carried out with a membrane of 12-14 kDa MWCO. Also, the ratio was improved by the use of ultrafiltration and diafiltration on the pilot-scale.

3/7/11
DIALOG(R)File 5:Biosis Previews(R)

16311227 BIOSIS NO.: 200100483066
The solution structure and heme binding of the presequence of murine 5-aminolevulinate synthase
AUTHOR: Goodfellow Brian J; Dias Jorge S; Ferreira Gloria C; Henklein Peter ; Wray Victor; Macedo Anjos L (Reprint)
AUTHOR ADDRESS: Departamento de Quimica, Faculdade de Ciencias e Tecnologia, C.Q.F.B., Universidade Nova de Lisboa, 2825-114, Caparica, Portugal**Portugal
JOURNAL: FEBS Letters 505 (2): p325-331 14 September, 2001 2001
MEDIUM: print
ISSN: 0014-5793
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The mitochondrial import of 5-aminolevulinate synthase (ALAS), the first enzyme of the mammalian heme biosynthetic pathway, requires the N-terminal presequence. The 49 amino acid presequence transit peptide (psALAS) for murine erythroid ALAS was chemically synthesized, and circular dichroism and 1H nuclear magnetic resonance (NMR) spectroscopies used to determine structural elements in trifluoroethanol/H2O solutions and micellar environments. A well defined amphipathic alpha-helix, spanning L22 to F33, was present in psALAS in 50% trifluoroethanol. Further, a short alpha-helix, defined by A5-L8, was also apparent in the 26 amino acid N-terminus peptide, when its structure was determined in sodium dodecyl sulfate. Heme inhibition of ALAS mitochondrial import has been reported to be mediated through cysteine residues in presequence heme regulatory motifs (HRMs). A UV/visible and 1H NMR study of hemin and psALAS indicated that a %%%heme%%%-%%%peptide%%% interaction occurs and demonstrates, for the first time, that heme interacts with the HRMs of psALAS.

3/7/12
DIALOG(R)File 5:Biosis Previews(R)

16147066 BIOSIS NO.: 200100318905
Calcium-dependent conformation of a heme and fingerprint peptide of the diheme cytochrome c peroxidase from Paracoccus pantotrophus
AUTHOR: Pauleta Sofia R; Lu Yi; Goodhew Celia F; Moura Isabel; Pettigrew Graham W; Shelnutt John A (Reprint)
AUTHOR ADDRESS: Biomolecular Materials and Interfaces Department, Sandia National Laboratories, Albuquerque, NM, 87185-1349, USA**USA
JOURNAL: Biochemistry 40 (22): p6570-6579 June 5, 2001 2001
MEDIUM: print
ISSN: 0006-2960
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The structural changes in the heme macrocycle and substituents

caused by binding of Ca2+ to the diheme cytochrome c peroxidase from Paracoccus pantotrophus were clarified by resonance Raman spectroscopy of the inactive fully oxidized form of the enzyme. The changes in the macrocycle vibrational modes are consistent with a Ca2+-dependent increase in the out-of-plane distortion of the low-potential heme, the proposed peroxidatic heme. Most of the increase in out-of-plane distortion occurs when the high-affinity site I is occupied, but a small further increase in distortion occurs when site II is also occupied by Ca2+ or Mg2+. This increase in the heme distortion explains the red shift in the Soret absorption band that occurs upon Ca2+ binding. Changes also occur in the low-frequency substituent modes of the heme, indicating that a structural change in the covalently attached fingerprint pentapeptide of the LP heme occurs upon Ca2+ binding to site I. These structural changes may lead to loss of the sixth ligand at the peroxidatic heme in the semireduced form of the enzyme and activation.

3/7/13
DIALOG(R)File 5:Biosis Previews(R)

15692309 BIOSIS NO.: 200000410622
Influence of the extent of haemoglobin hydrolysis on the digestive absorption of haem iron in the rat. An in vitro study
AUTHOR: Vaghefi N; Nedjaoum F; Guillochon D; Bureau F; Arhan P; Bougle D (Reprint)
AUTHOR ADDRESS: Laboratoire de Physiologie Digestive et Nutritionnelle, CHU, Avenue de la Cote de Nacre, 14033, Caen, France**France
JOURNAL: Experimental Physiology 85 (4): p379-385 July, 2000 2000
MEDIUM: print
ISSN: 0958-0670
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: This study was designed to assess the %%%haem%%%-%%%peptide%%% interactions which occur during progressive haemoglobin hydrolysis by digestive enzymes and their relationship with haem iron digestive absorption. The behaviour of different haemoglobin hydrolysates was studied using the Ussing chamber model. Hydrolysates were produced from enzyme digestion of bovine haemoglobin at pH 3 by pepsin and at pH 10 by subtilisin. Samples with increasing degrees of hydrolysis (0-15%) were studied. Biochemical assays (pyridine haemochromogen method and UV absorption spectra) were used to follow haem solubility and %%%haem%%%-%%%peptide%%% interactions in samples. Increasing the hydrolysis level of haemoglobin was associated with an enhanced iron uptake; the highest uptake rate was reached between 8 and 11% of globin hydrolysis, whichever enzyme was used. The mechanisms rendering iron soluble and available differ between the two enzymes. The comparison between biochemical and absorption data suggests that the formation of soluble peptide-haem complexes was not sufficient to enhance haem iron absorption, since globin-bound iron is poorly absorbed; an efficient absorption occurred only when haem was loosely bound to low molecular weight peptides.

3/7/14
DIALOG(R)File 5:Biosis Previews(R)

15613013 BIOSIS NO.: 200000331326
Use of heme-peptides to prevent or retard disease associated with oxidative stress
AUTHOR: Spector Abraham (Reprint); Ma Wanchao; Wang Ren-Rong
AUTHOR ADDRESS: New York, NY, USA**USA
JOURNAL: Official Gazette of the United States Patent and Trademark Office Patents 1230 (2): Jan. 11, 2000 2000
MEDIUM: e-file
ISSN: 0098-1133
DOCUMENT TYPE: Patent
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: This invention provides a method for treating a condition associated with oxidative stress in a subject which comprises administering to the subject an amount of a %%%heme%%%-%%%peptide%%% effective to treat the condition associated with oxidative stress in the subject. The subject may be a mammal. The mammal may be a human being. The condition associated with oxidative stress may be an inflammatory condition, an allergic condition or an auto-immune condition.

3/7/15
DIALOG(R)File 5:Biosis Previews(R)

15535595 BIOSIS NO.: 200000253908
Covalently modified microperoxidases as %%%heme%%%-%%%peptide%%% models for peroxidases
AUTHOR: Casella Luigi; De Gioia Luca; Frontoso Silvestri Grazia; Monzani Enrico (Reprint); Redaelli Cristina; Roncone Raffaella; Santagostini Laura
AUTHOR ADDRESS: Dipartimento di Chimica Generale, Universita di Pavia, Via Taramelli 12, 27100, Pavia, Italy**Italy
JOURNAL: Journal of Inorganic Biochemistry 79 (1-4): p31-39 April, 2000 2000
MEDIUM: print
ISSN: 0162-0134
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Microperoxidase-8 (MP8) and microperoxidase-9 (MP9) have been covalently modified by attachment of proline-containing residues to the amino terminal peptide chain in order to obtain new peroxidase model systems. The catalytic activities of these derivatives in the oxidation of p-cresol by hydrogen peroxide have been compared to that of MP8. The presence of steric hindrance above the heme reduces the formation rate of the catalytically active species, while the reactivity is increased when the amino group of a proline residue is close to the iron. The modification of the catalyst affects the rate of degradation processes undergone by the heme group during catalysis. A bulky aromatic group on the distal side decreases the stability of the complex because it reduces the mobility of a phenoxy radical species formed during catalysis, while the presence of proline residues increases the number of turnovers of the

heme catalysts before degradation. The complex Pro2-MP8 obtained by addition of two proline residues to MP8 exhibits the best catalytic performance in terms of activity and chemical stability.

3/7/16
DIALOG(R)File 5:Biosis Previews(R)

14927611 BIOSIS NO.: 199900187271
The hydrophobic lipid environment of a nickel-reconstituted %%%heme%%%-%%%peptide%%% influences porphyrin distortion
AUTHOR: Ma Jian-Guo (Reprint); Zhang Jun (Reprint); Jia Song-Ling (Reprint); Lu Yi (Reprint); Vanderkooi Jane M; Shelnutt John A (Reprint)
AUTHOR ADDRESS: New Materials and Validation Department, Sandia National Laboratories, Albuquerque, NM, 87185-1349, USA**USA
JOURNAL: Biophysical Journal 76 (1 PART 2): pA419 Jan., 1999 1999
MEDIUM: print
CONFERENCE/MEETING: Forty-third Annual Meeting of the Biophysical Society Baltimore, Maryland, USA February 13-17, 1999; 19990213
ISSN: 0006-3495
DOCUMENT TYPE: Meeting; Meeting Abstract; Meeting Poster
RECORD TYPE: Citation
LANGUAGE: English

3/7/17
DIALOG(R)File 5:Biosis Previews(R)

14796732 BIOSIS NO.: 199900056392
Solubility of heme in heme-iron enriched bovine hemoglobin hydrolysates
AUTHOR: Lebrun Frederic; Bazus Anne; Dhulster Pascal; Guillochon Didier (Reprint)
AUTHOR ADDRESS: Lab. Technol. Substances Nat., IUT "A" Lille I, BP 179, 59653 Villeneuve Ascq Cedex, France**France
JOURNAL: Journal of Agricultural and Food Chemistry 46 (12): p5017-5025 Dec., 1998 1998
MEDIUM: print
ISSN: 0021-8561
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A heme-iron enriched peptidic hydrolysate was prepared from bovine hemoglobin, at pilot plant scale, by peptic hydrolysis followed by ultrafiltration. Such preparations are attractive for iron deficiency therapy and have been reported in the literature in the context of utilization of blood in the food industry. The peptidic fraction of this hydrolysate was able to solubilize heme in higher proportion than hemoglobin even at acidic pH where heme is totally insoluble. One peptide, having a similar ability to solubilize heme in the same range of pH, was isolated from this fraction and taken as a model to investigate the mechanisms involved in heme solubilization. Heme seemed to be mainly solubilized through hydrophobic interactions with the peptide, whereas ligancies or electrostatic interaction could not be demonstrated. The stoichiometry of %%%heme%%%-%%%peptide%%% adducts depends on pH with a

2:2 association at pH 2 between heme as a dimer and two peptides and with a 2:1 association at pH 7.5 between one dimer and one single peptide. However, the existence of higher molecular weight aggregates cannot be excluded in the whole hemoglobin hydrolysate. Despite the good solubility of heme and the high heme/protein ratio, such heme enriched peptidic hydrolysates could have a weak bioavailability since heme polymerization is known to decrease heme-iron intestinal absorption. Further studies will be necessary to reduce heme polymerization during enzymatic hydrolysis of bovine hemoglobin.

3/7/18
DIALOG(R)File 5:Biosis Previews(R)

14791719 BIOSIS NO.: 199900051379
Identification of the heme-modified peptides from cumene hydroperoxide-inactivated cytochrome P450 3A4
AUTHOR: He Kan; Bornheim Lester M; Falick Arnold M; Maltby David; Yin Hequn ; Correia Maria Almira (Reprint)
AUTHOR ADDRESS: Dep. Cellular Molecular Pharmacology, Univ. Calif., San Francisco, CA 94143, USA**USA
JOURNAL: Biochemistry 37 (50): p17448-17457 Dec. 15, 1998 1998
MEDIUM: print
ISSN: 0006-2960
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Cumene hydroperoxide-mediated (CuOOH-mediated) inactivation of cytochromes P450 (CYPs) results in destruction of their prosthetic heme to reactive fragments that irreversibly bind to the protein. We have attempted to characterize this process structurally, using purified, 14C-heme labeled, recombinant human liver P450 3A4 as the target of CuOOH-mediated inactivation, and a battery of protein characterization approaches (chemical (CNBr) and proteolytic (lysylendopeptidase-C) digestion, HPLC-peptide mapping, microEdman sequencing, and mass spectrometric analyses). The %%%heme%%%-%%%peptide%%% adducts isolated after CNBr/lysylendopeptidase-C digestion of the CuOOH-inactivated P450 3A4 pertain to two distinct P450 3A4 active site domains. One of the peptides isolated corresponds to the proximal helix L-Cys-region peptide 429-450 domain and the others to the K-region (peptide 359-386 domain). Although the precise residue(s) targeted remain to be identified, we have narrowed down the region of attack to within a 17 amino acid peptide (429-445) stretch of the 55-amino acid proximal helix L/Cys domain. Furthermore, although the exact structures of the heme-modifying fragments and the nature of the adduction remain to be established conclusively, the incremental masses of apprxeq302 and 314 Da detected by electrospray mass spectrometric analyses of the heme-modified peptides are consistent with a dipyrrolic heme fragment comprised of either pyrrole ring A-D or B-C, a known soluble product of peroxidative heme degradation, as a modifying species.

3/7/19
DIALOG(R)File 5:Biosis Previews(R)

14710853 BIOSIS NO.: 199800505100
New synthetic tools for peptide-tetraphenylporphyrin derivatives
AUTHOR: de Luca Stefania; Bruno Giovanni; Fattorusso Roberto; Isernia Carla ; Pedone Carlo; Morelli Giancarlo (Reprint)
AUTHOR ADDRESS: Centro Interuniversitario Ricerca Peptidi Bioattivi, CNR, Via Mezzocannone 4, I-80134 Napoli, Italy**Italy
JOURNAL: Letters in Peptide Science 5 (4): p269-276 July, 1998 1998
MEDIUM: print
ISSN: 0929-5666
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: New metal-tetraphenylporphyrins and Fmoc-lysine-metalloporphyrin derivatives have been used to prepare peptide-porphyrin and peptide-metalloporphyrin compounds via solid-phase peptide synthesis. A water-soluble peptide, covalently bound to a manganese(III)-porphyrin, has been used as a catalyst to promote the oxidation of ABTS by hydrogen peroxide or t-butylhydroperoxide.

3/7/20
DIALOG(R)File 5:Biosis Previews(R)

14652519 BIOSIS NO.: 199800446766
The structural origin of nonplanar heme distortions in tetraheme ferricytochromes c3
AUTHOR: Ma Jian-Guo; Zhang Jun; Franco Ricardo; Jia Song-Ling; Moura Isabel ; Moura Jose J G; Kroneck Peter M H; Shelnutt John A (Reprint)
AUTHOR ADDRESS: Materials Theory Computation Dep., Sandia Natl. Lab., Albuquerque, NM 87185-1349, USA**USA
JOURNAL: Biochemistry 37 (36): p12431-12442 Sept. 8, 1998 1998
MEDIUM: print
ISSN: 0006-2960
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Resonance Raman (RR) spectroscopy, molecular mechanics (MM) calculations, and normal-coordinate structural decomposition (NSD) have been used to investigate the conformational differences in the hemes in ferricytochromes c3. NSD analyses of heme structures obtained from X-ray crystallography and MM calculations of %%%heme%%%-%%%peptide%%% fragments of the cytochromes c3 indicate that the nonplanarity of the hemes is largely controlled by a fingerprint peptide segment consisting of two heme-linked cysteines, the amino acids between the cysteines, and the proximal histidine ligand. Additional interactions between the heme and the distal histidine ligand and between the heme propionates and the protein also influence the heme conformation, but to a lesser extent than the fingerprint peptide segment. In addition, factors that influence the folding pattern of the fingerprint peptide segment may have an effect on the heme conformation. Large heme structural differences between the baculatum cytochromes c3 and the other proteins are uncovered by the NSD procedure (Jentzen, W., Ma, J.-G., and Shelnutt, J. A. (1998) Biophys. J. 74, 753-763). These heme differences are mainly associated with the

deletion of two residues in the covalently linked segment of hemes 4 for the baculatum proteins. Furthermore, some of these structural differences are reflected in the RR spectra. For example, the frequencies of the structure-sensitive lines (nu4, nu3, and nu2) in the high-frequency region of the RR spectra are lower for the Desulfomicrobium baculatum cytochromes c3 (Norway 4 and 9974) than for the Desulfovibrio (D.) gigas, D. vulgaris, and D. desulfuricans strains, consistent with a more ruffled heme. Spectral decompositions of the nu3 and nu10 lines allow the assignment of the sublines to individual hemes and show that ruffling, not saddling, is the dominant factor influencing the frequencies of the structure-sensitive Raman lines. The distinctive spectra of the baculatum strains investigated are a consequence of hemes 2 and 4 being more ruffled than is typical of the other proteins.

3/7/21
DIALOG(R)File 5:Biosis Previews(R)

14331031 BIOSIS NO.: 199800125278
Synthetic peptides corresponding to a repetitive sequence of malarial histidine rich protein bind haem and inhibit haemozoin formation in vitro
AUTHOR: Pandey Amit V; Joshi Ratanmani; Tekwani Babu L (Reprint); Singh Ram L; Chauhan Virender S
AUTHOR ADDRESS: Div. Biochem., Cent. Drug Res. Inst., Lucknow 226001, India **India
JOURNAL: Molecular and Biochemical Parasitology 90 (1): p281-287 Dec. 1, 1997 1997
MEDIUM: print
ISSN: 0166-6851
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Synthetic peptides containing a repetitive hexapeptide sequence (Ala-His-His-Ala-Ala-Asp) of malarial histidine-rich protein II were evaluated for binding with haem in vitro. The pattern of haem binding suggested that each repeat unit of this sequence provides one binding site for haem. Chloroquine inhibited the %%%haem%%%-%%%peptide%%% complex formation with preferential formation of a haem-chloroquine complex. In vitro studies on haem polymerization showed that none of the peptides could initiate haemozoin formation. However, they could inhibit haemozoin formation promoted by a malarial parasite extract, possibly by competitively binding free haem. These results indicate this hexapeptide sequence represents the haem binding site of the malarial histidine-rich protein and possibly the site of nucleation for haem polymerization.

3/7/22
DIALOG(R)File 5:Biosis Previews(R)

13322209 BIOSIS NO.: 199698790042
Isolation and characterization of the d-1 domain of Pseudomonas aeruginosa nitrite reductase
AUTHOR: Silvestrini Maria Chiara (Reprint); Cutruzzola Francesca; Schinina Maria Eugenia; Maras Bruno; Rolli Gabriella; Brunori Maurizio

AUTHOR ADDRESS: Dipartimento di Scienze Biochimiche, Universita di Roma La Sapienza, P.le A. Moro, 5, 00185 Rome, Italy**Italy
JOURNAL: Journal of Inorganic Biochemistry 62 (2): p77-87 1996 1996
ISSN: 0162-0134
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Proteolitic digestion of nitrite reductase from Pseudomonas aeruginosa allows to obtain and purify a domain containing only the d, heme and constituted by two noncovalently bound peptides. This d-1 domain catalyzes oxygen consumption, and binds carbon monoxide with a kinetic constant slightly higher than the parental dimeric holoenzyme. The capacity to oxidize the physiological substrate, cytochrome C-551, is lost, even when the proteolytic c heme domain is added to this reaction mixture. This finding suggests that the two domains do not have a significant affinity for each other, and are kept together only by being part of the same polypeptide.

13258386 BIOSIS NO.: 199698726219
H-NMR study of temperature-induced structure alteration at the active site of horse heart cytochrome
AUTHOR: Yamamoto Yasuhiko
AUTHOR ADDRESS: Dep. Chem., Univ. Tsukuba, Tsukuba, Ibaraki 305, Japan** Japan
JOURNAL: Journal of Biochemistry (Tokyo) 119 (1): p16-22 1996 1996
ISSN: 0021-924X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The molecular structure of the active site of horse heart met-cyano cytochrome c, as a function of temperature, has been investigated using 1H-NMR. A temperature dependence study of the NMR spectra revealed that one heme methyl proton resonance exhibits anti-Curie behavior, ie., the hyperfine shift increases with increasing temperature. Analyses of the average heme methyl proton hyperfine shift and the proximal His imidazole proton resonances indicated that the iron-His bonding interaction in this protein is essentially independent of temperature. Since such an anomalous temperature dependence of the heme methyl proton resonance disappears in met-cyano complex of a %%%heme%%% %%%peptide%%% prepared by enzymatic degradation of the protein (Smith, M. and McLendon, G. (1981) J. Am. Chem. Soc. 103, 4912-4921), the anti-Curie behavior observed for the heme methyl proton resonance in met-cyano cytochrome c is attributed to a rotational displacement of the heme about the iron-His bond relative to the protein moiety due to a temperature-dependent conformational alteration of the heme-protein linkage. Such rotational mobility of heme at the active site of a protein may be responsible for the anomalous temperature dependence of heme methyl proton hyperfine shifts reported for many c-type ferri cytochromes.

3/7/24
DIALOG(R)File 5:Biosis Previews(R)

13135378 BIOSIS NO.: 199698603211
Monomeric ferric %%%heme%%% %%%peptide%%% derivatives: Model systems for hemoproteins
AUTHOR: Carraway Angela D; Povlock Sue L; Houston Melinda L; Johnston David S; Peterson Jim (Reprint)
AUTHOR ADDRESS: Dep. Chem., Univ. Alabama, Tuscaloosa, AL 35487-0336, USA** USA
JOURNAL: Journal of Inorganic Biochemistry 60 (4): p267-276 1995 1995
ISSN: 0162-0134
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Electron paramagnetic resonance spectra of a number of ferric %%%heme%%% %%%peptide%%% derivatives, in aqueous-detergent and various aqueous-alcohol solvent mixtures, have been obtained using samples in the concentration range 0.1-1.0 mM. Some of these were clearly monomeric, homogeneous, mixed-ligand adducts, entirely suitable for use as model systems for hemoprotein spectroscopic studies. As anticipated, the measured EPR parameters were largely independent of solvent environment. Surprisingly, micellar preparations of ferric heme undecapeptide in mildly alkaline solution showed no evidence for the formation of a hydroxide adduct, contrary to a previous report (S. Mazumdar, O. K. Medhi and S. Mitra, Inorg. Chem. 30 700 (1991)).
? ds

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Set     Items   Description
S1          0   ((HEME OR HAEM)()?PEPTIDE?)
S2          0   ((HEME OR HAEM)()?PEPTIDE)
S3        104   ((HEME OR HAEM)()PEPTIDE)
? s s3 and cysteine
            104  S3
          69475  CYSTEINE
      S4      6  S3 AND CYSTEINE
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? t s4/7/1-6

4/7/1
DIALOG(R)File 5:Biosis Previews(R)

18471933 BIOSIS NO.: 200510166433
Iron absorption from concentrated hemoglobin hydrolysate by rat
AUTHOR: Vaghefi Nikta; Nedjaoum Fuzia; Guillochon Didier; Bureau Francois; Arhan Pierre; Bougle Dominique (Reprint)
AUTHOR ADDRESS: CHU Caen, Lab Physiol Digest and Nutritionnelle, F-14033 Caen, France**France
AUTHOR E-MAIL ADDRESS: bougle-d@chu-caen.fr
JOURNAL: Journal of Nutritional Biochemistry 16 (6): p347-352 JUN 2005 2005
ISSN: 0955-2863
DOCUMENT TYPE: Article
RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Although heme iron is highly bioavailable, the low iron content of hemoglobin prevents its use for dietary fortification; on the other hand, purified heme has low solubility and absorption rate. The present study was designed to assess the interactions between concentrated heme iron and peptides released during globin hydrolysis and %%%cysteine%%% and their relation with iron absorption.Hemoglobin was hydrolyzed by pepsin or subtilisin, and then, heme iron was concentrated by ultrafiltration. Iron absorption was studied in a Ussing chamber; gluconate was used as control. Iron uptake from nonconcentrated pepsin hydrolysate and gluconate was lower than from other groups. %%%Cysteine%%% significantly enhanced iron uptake except from the concentrated subtilisin hydrolysate. There was no significant difference between %%%cysteine%%%-supplemented groups.According to the different hydrolysis pathways of enzymes, it is assumed that the presence of hydrophobic peptides and the strength of %%%heme%%%-%%%peptide%%% interactions are both determining factors of heme iron absorption. These interactions occur mainly before iron uptake, as emphasized by the effect of %%%cysteine%%%.

4/7/2
DIALOG(R)File 5:Biosis Previews(R)

16311227 BIOSIS NO.: 200100483066
The solution structure and heme binding of the presequence of murine 5-aminolevulinate synthase
AUTHOR: Goodfellow Brian J; Dias Jorge S; Ferreira Gloria C; Henklein Peter ; Wray Victor; Macedo Anjos L (Reprint)
AUTHOR ADDRESS: Departamento de Quimica, Faculdade de Ciencias e Tecnologia, C.Q.F.B., Universidade Nova de Lisboa, 2825-114, Caparica, Portugal**Portugal
JOURNAL: FEBS Letters 505 (2): p325-331 14 September, 2001 2001
MEDIUM: print
ISSN: 0014-5793
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The mitochondrial import of 5-aminolevulinate synthase (ALAS), the first enzyme of the mammalian heme biosynthetic pathway, requires the N-terminal presequence. The 49 amino acid presequence transit peptide (psALAS) for murine erythroid ALAS was chemically synthesized, and circular dichroism and 1H nuclear magnetic resonance (NMR) spectroscopies used to determine structural elements in trifluoroethanol/H2O solutions and micellar environments. A well defined amphipathic alpha-helix, spanning L22 to F33, was present in psALAS in 50% trifluoroethanol. Further, a short alpha-helix, defined by A5-L8, was also apparent in the 26 amino acid N-terminus peptide, when its structure was determined in sodium dodecyl sulfate. Heme inhibition of ALAS mitochondrial import has been reported to be mediated through %%%cysteine%%% residues in presequence heme regulatory motifs (HRMs). A UV/visible and 1H NMR study of hemin and psALAS indicated that a %%%heme%%%-%%%peptide%%% interaction occurs and demonstrates, for the first time, that heme interacts with the HRMs of psALAS.

4/7/3
DIALOG(R)File 5:Biosis Previews(R)

07730466 BIOSIS NO.: 198580039361
IDENTIFICATION OF THE BINDING SITE ON CYTOCHROME C-1 FOR CYTOCHROME C
AUTHOR: STONEHUERNER J (Reprint); O'BRIEN P; GEREN L; MILLETT F; STEIDL J; YU L; YU C-A
AUTHOR ADDRESS: DEPARTMENT CHEMISTRY, UNIVERSITY ARKANSAS, FAYETTEVILLE, ARKANSAS 72701, USA**USA
JOURNAL: Journal of Biological Chemistry 260 (9): p5392-5398 1985
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The reagent 1-ethyl-3-(3-[14C]trimethylaminopropyl)carbodiimide (ETC) was used to identify specific carboxyl groups on the horse heart cytochrome bc1 complex (ubiquinol-cytochrome c reductase, EC 1.10.2.2) involved in binding cytochrome c. Treatment of the cytochrome bc1 complex with 2 mM ETC led to inhibition of the electron transfer activity with cytochrome c. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis indicated that both the cytochrome c1 %%%heme%%% %%%peptide%%% and the MW = 9175 hinge peptide were radiolabeled by ETC. In addition, a new band appeared at a position consistent with a 1:1 cross-linked cytochrome c1-hinge peptide species. Treatment of a 1:1 cytochrome bc1-cytochrome c complex with ETC led to the same inhibition of electron transfer activity observed with the uncomplexed cytochrome bc1, but to decreased radiolabeling of the cytochrome c1 %%%heme%%% %%%peptide%%%. Two new cross-linked species corresponding to cytochrome c-hinge peptide and cytochrome c-cytochrome c1 were formed in place of the cytochrome c1-hinge peptide species. To identify the specific carboxyl groups labeled by ETC, a purified cytochrome c1 preparation containing both the %%%heme%%% %%%peptide%%% and the hinge peptide was dimethylated at all the lysines to prevent internal cross-linking. The methylated cytochrome c1 preparation was treated with ETC and digested with trypsin and chymotrypsin, and the resulting peptides were separated by high pressure liquid chromatography. ETC labeled the cytochrome c1 peptides 63-81, 121-128 and 153-179 and the hinge peptides 1-17 and 48-65. All of these peptides are highly acidic and contain one or more regions of adjacent carboxyl groups. The only peptide consistently protected from labeling by cytochrome c binding was 63-81, demonstrating that the carboxyl groups at residues 66, 67, 76, and 77 are involved in binding cytochrome c. These residues are relatively close to the heme-binding %%%cysteine%%% residues 37 and 40 and indicate a possible site for electron transfer from cytochrome c1 to cytochrome c.

4/7/4
DIALOG(R)File 5:Biosis Previews(R)

06926450 BIOSIS NO.: 198376017885
THE INTERACTION BETWEEN HEME AND PROTEIN IN CYTOCHROME C-1
AUTHOR: TERVOORT M J (Reprint); VAN GELDER B F

AUTHOR ADDRESS: LAB BIOCHEMISTRY, BCP JANSEN INSTITUTE, UNIV AMSTERDAM, PO BOX 20151, 1000 HD AMSTERDAM**NETHERLANDS
JOURNAL: Biochimica et Biophysica Acta 722 (1): p137-143 1983
ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The optical spectrum of reduced bovine [heart] cytochrome c1 at 77.degree. K shows a fine splitting of the .beta.-band, which is indicative of the native conformation of the protein. At room temperature, this conformation is reflected in an absorbance band at 530 nm. The exposure of the heme of ferrocytochrome c1, investigated by solvent-perturbation spectroscopy, appears to be extremely sensitive to temperature and SH reagents, bound to the oxidized protein. Addition of combinations of potential ligands to the isolated tryptic %%%heme%%% %%%peptide%%% of cytochrome c1 reveals that only a mixture of methionine and %%%cysteine%%% (or their equivalents) generates a .beta.-band at 77.degree. K which is identical in shape to that of native cytochrome c1. In the EPR spectrum of a complex of ferrocytochrome c1 and nitric oxide at pH 10.5, no hyperfine splitting derived from a second ligated N atom could be detected. The results indicate that methionine and %%%cysteine%%% are the axial ligands of heme in cytochrome c1. The EPR spectrum of isolated ferricytochrome c1 is that of a low-spin heme iron compound with a gz value of 3.36 and a gy value of 2.04.

4/7/5
DIALOG(R)File 5:Biosis Previews(R)

05732078 BIOSIS NO.: 197968043577
THE AMINO-ACID SEQUENCE OF CYTOCHROME C-PRIME FROM THE PURPLE SULFUR BACTERIUM CHROMATIUM-VINOSUM
AUTHOR: AMBLER R P (Reprint); DANIEL M; MEYER T E; BARTSCH R G; KAMEN M D
AUTHOR ADDRESS: DEP MOL BIOL, UNIV EDINB, EDINBURGH EH9 3JR, SCOTL, UK**UK
JOURNAL: Biochemical Journal 177 (3): p819-824 1979
ISSN: 0264-6021
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: An amino acid sequence is proposed for the cytochrome c' from the photosynthetic purple sulphur bacterium C. vinosum strain D. It is a single polypeptide chain of 131 residues, with heme-attachment %%%cysteine%%% residues at positions 121 and 124. The results discredit an earlier report of a di-%%%heme%%% %%%peptide%%% sequence from this protein. The sequence belongs to the same class as the published Alcaligenes and Rhodospirillum rubrum cytochrome c' sequences, but the resemblance is not close.

4/7/6
DIALOG(R)File 5:Biosis Previews(R)

05100501 BIOSIS NO.: 197763021357

ELECTRON TRANSPORT SYSTEMS IN KINETOPLASTIDA
AUTHOR: HILL G C
JOURNAL: Biochimica et Biophysica Acta 456 (2): p149-193 1976
ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: Cyanide-sensitive trypanosomatids have an electron transport system which includes cytochromes b, c1, c, aa3, and coenzyme Q9. The cytochromes c present in trypanosomatids are atypical, with an .alpha.-peak from 555-558 nm in the reduced form. Only 1 %%%cysteine%%% residue is present in the %%%heme%%% %%%peptide%%% region linking the protein to the prosthetic group. The prosthetic group is probably a monosubstituted protoheme IX with 1 unsaturated vinyl group. Some cyanide-sensitive trypanosomatids (e.g. Trypanosoma mega, L. tarentolae) have demonstrated action spectral evidence for 2 terminal oxidases present, cytochrome aa3 and cytochrome o. A branched electron transport system has been proposed for cyanide-sensitive trypanosomatids, with cytochrome aa3 as 1 oxidase and cytochrome o as an alternative oxidase. Salivarian trypanosomes grown in culture initially develop succinate oxidation which is cyanide insensitive. Some insect trypanosomatids have a high percentage of succinate cyanide-insensitive oxidation e.g., T. mega with 50% KCN insensitivity. The identity of the oxidase which has an intermediate sensitivity to KCN in comparison to cytochrome aa3, or the L-.alpha.-glycerophosphate oxidase, is not known. Bloodstream forms of African trypanosomes have a cyanide-insensitive L-.alpha.-glycerophosphate oxidase system. The system consists of 2 components, the particulate L-.alpha.-glycerophosphate dehydrogenase and the particulate L-.alpha.-glycerophosphate oxidase. The oxidase is inhibited by aromatic hydroxamic acids and the trypanocidal drug suramin.

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? s (Cys()Ala()Ala()Cys)
          15333  CYS
          28026  ALA
          28026  ALA
          15333  CYS
     S7      20  (CYS()ALA()ALA()CYS)
? t s7/7/1-20
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7/7/1
DIALOG(R)File 5:Biosis Previews(R)

0019537140 BIOSIS NO.: 200700196881
Receptor-mediated internalization of chelator-PNA-peptide hybridization probes for radioimaging or magnetic resonance imaging of oncogene mRNAs in tumours
AUTHOR: Tian X; Chakrabarti A; Amirkhanov N; Aruva M R; Zhang K; Cardi C A; Lai S; Thakur M L; Wickstrom E (Reprint)
AUTHOR ADDRESS: Thomas Jefferson Univ, Dept Biochem and Mol Biol, Philadelphia, PA 19107 USA**USA
AUTHOR E-MAIL ADDRESS: eric@tesla.jci.tju.edu
JOURNAL: Biochemical Society Transactions 35 (Part 1): p72-76 FEB 2007 2007
ISSN: 0300-5127
DOCUMENT TYPE: Article

RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Early external detection of cancer gene activity might enable early treatment of cancer and might reduce cancer mortality. We hypothesized that oncogene mRNA overexpressed at thousands of copies per malignant cell in a zone of transformed cells could be imaged externally by scintigraphic imaging, PET (positron emission tomography) or MRI (magnetic resonance imaging) with PNA (peptide nucleic acid) hybridization probes that include chelators for metal cations and a cyclized peptide analogue of IGF-1 (insulin-like growth factor 1), D(Cys-Ser-Lys-Cys), to mediate internalization by IGF1R (IGF-1 receptor) overexpressed on cancer cells. We observed that human MCF7 breast cancer cells that overexpress IGF1R efficiently internalized fluorescein-chelator-PNA-D(Cys-Ser-Lys-Cys) to the cytoplasm, but not with D(%%%Cys%%%-%%%Ala%%%-%%%Ala%%%-%%%Cys%%%). Scintigraphic imaging of MCF7 xenografts in immunocompromised mice revealed that CCND1 and MYC [Tc-99m]chelator-PNA-D(Cys-Ser-Lys-Cys) probes yielded xenograft. PET imaging with [Cu-64]chelator-PNA-D(Cys-Ser-Lys-Cys) yielded stronger signals. Scintigraphic imaging of human AsPC1 pancreas cancer xenografts with [Tc-99m]chelator-KRAS PNA-D(Cys-Ser-Lys-Cys) yielded strong xenograft signals. Stronger xenograft image intensities were obtained by PET imaging of [Cu-64]chelator-KRAS PNA-D(Cys-Ser-Lys-Cys). MRI required extension of chelator- polydiamidopropanoate dendrimers from the N-termini of the PNA probes to increase the number of contrast paramagnetic gadolinium (III) cations per probe. These results provide a basis for detection of oncogene activity in tissues from outside the body by hybridization with metal-chelator-PNA-peptides that are selectively internalized by cancer cells.

7/7/2
DIALOG(R)File 5:Biosis Previews(R)

18772450 BIOSIS NO.: 200600117845
Intramolecular electron transfer between tyrosyl radical and cysteine residue inhibits tyrosine nitration and induces thiyl radical formation in model peptides treated with myeloperoxidase, H2O2, and NO2- - EPR spin trapping studies
AUTHOR: Zhang Hao; Xu Yingkai; Joseph Joy; Kalyanaraman B (Reprint)
AUTHOR ADDRESS: Med Coll Wisconsin, Dept Biophys, 8701 Watertown Plank Rd,POB 26509, Milwaukee, WI 53226 USA**USA
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JOURNAL: Journal of Biological Chemistry 280 (49): p40684-40698 DEC 9 2005 2005
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We investigated the effects of a cysteine residue on tyrosine nitration in several model peptides treated with myeloperoxidase (MPO), H2O2, and nitrite anion (NO2-) and with horseradish peroxidase and H2O2. Sequences of model peptides were acetyl-Tyr-Cys-amide(YC), acetyl-Tyr-Ala-Cys-amide(YAC), acetyl-Tyr-%%%Ala%%%-%%%Ala%%%-%%%Cys%%%-amide(YAAC), and acetyl-Tyr-Ala-Ala-%%%Ala%%%-%%%Ala%%%-%%%Cys%%%-amide(YAAAAC).

Results indicate that nitration and oxidation products of tyrosyl residue in YC and other model peptides were barely detectable. Amajorproductdetected was the corresponding disulfide (e. g. YCysCysY). Spin trapping experiments with 5,5'-dimethyl-1-pyrrolineN-oxide(DMPO) revealed thiyl adduct (e. g. DMPO-SCys-Tyr) formation from peptides (e. g. YC) treated withMPO/H2O2 and MPO/H2O2/NO2-. The steady-state concentrations of DMPO-thiyl adducts decreased with increasing chain length of model peptides. Blocking the sulfydryl group in YC with methylmethanethiosulfonate(that formed YCSSCH3) totally inhibited thiyl radical formation as did substitution of Tyr with Phe (i.e. FC) in the presence of MPO/H2O2/NO2-. However, increased tyrosine nitration, tyrosine dimerization, and tyrosyl radical formation were detected in theMPO/H2O2/NO2-/YCSSCH3 system. Increased formation of S-nitrosated YC(YCysNO) was detected in the MPO/H2O2/(NO)-N-center dot system. We conclude that a rapid intramolecular electron transfer reaction between the tyrosyl radical and the Cys residue impedes tyrosine nitration and induces corresponding thiyl radical and nitrosocysteine product. Implications of this novel intramolecular electron transfer mechanism in protein nitration and nitrosation are discussed.

7/7/3
DIALOG(R)File 5:Biosis Previews(R)

11886054 BIOSIS NO.: 199396050470
Covalent modification with concomitant inactivation of the cAMP-dependent protein kinase by affinity labels containing only L-amino acids
AUTHOR: Salerno Allen; Lawrence David S (Reprint)
AUTHOR ADDRESS: Dep. Chem., State University New York, Buffalo, NY 14214, USA**USA
JOURNAL: Journal of Biological Chemistry 268 (18): p13043-13049 1993
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Affinity labels for proteins that process other proteins (e.g. proteinases and protein kinases) are an amalgam of two components, an active site-directed peptide carrier and a nonpeptidic electrophilic appendage. We have synthesized several affinity labels for the cAMP-dependent protein kinase that are composed solely of L-amino acids and therefore contain only functionality present in naturally occurring proteins. We have found that 2 adjacent cysteine residues, when covalently linked via a peptide bond and an intramolecular disulfide loop (abbreviated as Cys dblarw Cys), serves as a potent electrophile. The peptides Leu-Arg-Arg-Cys dblarw Cys-Leu-Gly (1), Leu-Arg-Arg-Ala-Cys dblarw Cys-Gly (2), and Leu-Arg-Arg-%%%Ala%%%-%%%Ala%%%-%%%Cys%%% dblarw Cys-Gly (3) inactivate the cAMP-dependent protein kinase in a time-dependent fashion. Since dialysis does not restore activity, but dithiothreitol does, this strongly suggests that covalent modification of the target enzyme has occurred at a cysteine residue. Although there are 2 cysteine moieties contained within the protein kinase, the 14C-acetylated affinity labels modify the enzyme only once. In addition, since ATP blocks inactivation of the protein kinase, this implies that it is the active site cysteine residue (Cys-199) that has undergone covalent modification. Based on the K-I(inact) values obtained from inactivation

kinetics, we conclude that the optimal site on the affinity label for the electrophilic Cys dblarw Cys is 1 amino acid removed from the 2 arginine residues (i.e. 2). In addition, the efficacy of these inhibitors is also dependent upon the size of the disulfide ring. The eight-membered disulfide ring-containing peptides 1-3 are relatively poor affinity labels compared to the 12-membered ring-containing inhibitor.

7/7/4
DIALOG(R)File 5:Biosis Previews(R)

11863215 BIOSIS NO.: 199396027631
Molecular cloning, nucleotide sequence, and characterization of lppB, encoding an antigenic 40-kilodalton lipoprotein of Haemophilus somnus
AUTHOR: Theisen Michael; Rioux Clement R (Reprint); Potter Andrew A
AUTHOR ADDRESS: Veterinary Infectious Disease Organization, Canadian Bacterial Diseases Network, 124 Veterinary Road, Univ. Saskatchewan, Saskatoon, Saskatchewan, Canada S7N OWO, canada**canada
JOURNAL: Infection and Immunity 61 (5): p1793-1798 1993
ISSN: 0019-9567
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Haemophilus somnus is a facultative intracellular pathogen which causes a wide range of diseases in cattle. To identify putative virulence determinants, a genomic library of H. somnus in Escherichia coli was screened for Congo red binding, a property associated with virulence in pathogenic bacteria, and subsequently with bovine hyperimmune sera raised against H. somnus HS25. A Congo red-binding clone carrying a 1.8-kb DNA insert was found to encode a strongly seroreactive LppB protein with an apparent molecular weight of 40,000. The nucleotide sequence of the entire DNA insert was determined. Two open reading frames coding for polypeptides with calculated molecular weights of 21,893 and 30,721 were identified. The larger open reading frame encoded LppB, while the smaller reading frame encoded a nonseroreactive protein with a relative molecular mass of approximately 18 kDa. The 16 amino-terminal amino acids of the deduced LppB polypeptide showed strong sequence homology to the signal peptide of secreted bacterial proteins, and the sequence Leu-%%%Ala%%%-%%%Ala%%%-%%%Cys%%% at the putative cleavage site corresponds to the consensus cleavage sequence of bacterial lipoproteins. Synthesis of the mature LppB lipoprotein in H. somnus was inhibited by globomycin, a specific inhibitor of signal peptidase II. LppB was localized to the outer membrane of H. somnus.

7/7/5
DIALOG(R)File 5:Biosis Previews(R)

11726638 BIOSIS NO.: 199395028904
The major anaerobically induced outer membrane protein of Neisseria gonorrhoeae, Pan 1, is a lipoprotein
AUTHOR: Hoehn Gerard T; Clark Virginia L (Reprint)
AUTHOR ADDRESS: Dep. Microbiol. Immunol., Sch. Med. Dentistry, Univ. Rochester, Rochester, N.Y. 14642, USA**USA

JOURNAL: Infection and Immunity 60 (11): p4704-4708 1992
ISSN: 0019-9567
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Pan 1 is an acidic outer membrane protein of Neisseria gonorrhoeae that is expressed only when gonococci are grown anaerobically. On silver-stained sodium dodecyl sulfate-polyacrylamide gels, Pan 1 migrates as an intense but diffuse 54-kDa protein. The deduced amino acid sequence of Pan 1 from the aniA (anaerobically induced protein) open reading frame reveals a lipoprotein consensus sequence, Ala-Leu-%%%Ala%%%-%%%Ala%%%-%%%Cys%%%, and a processed molecular mass of 39 kDa. Furthermore, there is strong homology at the N terminus and C terminus of Pan 1 to the termini of the gonococcal outer membrane lipoproteins Lip and Laz. (3H)palmitic acid labeling of gonococci grown under oxygen-limited conditions demonstrated specific incorporation of label into Pan 1, suggesting further that Pan 1 is a lipoprotein.

7/7/6
DIALOG(R)File 5:Biosis Previews(R)

11345446 BIOSIS NO.: 199294047287
METAL BINDING AND FOLDING PROPERTIES OF A MINIMALIST CYS-2HIS-2 ZINC FINGER PEPTIDE
AUTHOR: MICHAEL S F (Reprint); KILFOIL V J; SCHMIDT M H; AMANN B T; BERG J M
AUTHOR ADDRESS: DEP CHEMISTRY, JOHNS HOPKINS UNIVERSITY, 34TH CHARLES STREETS, BALTIMORE, MD 21210, USA**USA
JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 89 (11): p4796-4800 1992
ISSN: 0027-8424
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A minimalist Cys2 His2 zinc finger peptide, Lys-Tyr-Ala-%%%Cys%%%-%%%Ala%%%-%%%Ala%%%-%%%Cys%%%
-Ala-Ala-Ala-Phe-Ala-Ala-Lys-Ala-Ala-Leu-Ala-Ala-His-Ala-Ala-Ala-His-Ala-Lys, has been synthesized. Metal binding studies using Co2+ as a probe indicated that this peptide forms a 1:1 peptide/metal complex with a dissociation constant comparable to that observed for other zinc finger peptides. At high peptide concentrations, a 2:1 peptide/metal complex also forms, with four cysteinates coordinated to Co2+. Additional studies with sequence variants in which the canonical hydrophobic residues were changed to alanine, or in which one of the residues between the cysteines and the histidines was deleted, revealed an even more pronounced formation of the 2:1 complex over the 1:1 complex. In addition, the absorption spectra of the 1:1 peptide/Co2+ complexes of the variant peptides are significantly different from those seen for complexes of the parent peptide or those of more typical zinc finger peptides. NMR studies revealed that the parent peptide folds in the presence of Zn2+ to a structure very similar to that observed for other zinc finger peptides of this class. Taken together, these results suggest that the metal-binding and canonical hydrophobic residues are necessary and sufficient to

determine the structure of this class of zinc finger peptides.

7/7/7
DIALOG(R)File 5:Biosis Previews(R)

11269901 BIOSIS NO.: 199293112792
MOLECULAR CLONING NUCLEOTIDE SEQUENCE AND CHARACTERIZATION OF 40000-MOLECULAR-WEIGHT LIPOPROTEIN OF HAEMOPHILUS-SOMNUS
AUTHOR: THEISEN M (Reprint); RIOUX C R; POTTER A A
AUTHOR ADDRESS: STATENS SERUMINST, ARTILLERIVES 5, DK-2300 COPENHAGEN, DEN **DENMARK
JOURNAL: Infection and Immunity 60 (3): p826-831 1992
ISSN: 0019-9567
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A gene of Haemophilus somnus encoding the major 40,000-molecular-weight antigen (LppA) was cloned on a 2-kb Sau3AI fragment. The nucleotide sequence of the entire DNA insert was determined. One open reading frame, encoding a 247-residue polypeptide with a calculated molecular weight of 27,072, was identified. This reading frame was confirmed by sequencing the fusion joint of two independent IppA::TnphoA gene fusions. The 21 amino-terminal amino acids of the deduced polypeptide showed strong sequence homology to the signal peptide of secreted proteins, and the sequence Leu-Leu-%%%Ala%%%-%%%Ala%%%-%%%Cys%%% at the putative cleavage site is identical to the consensus cleavage sequence of lipoproteins from gram-negative bacteria. The presence of the lipid moiety on the protein was shown by incorporation of radioactive palmitic acid into the natural H. somnus protein. Palmitic acid could also be incorporated into the recombinant protein in Escherichia coli. Synthesis of the mature LppA lipoprotein was inhibited by globomycin, showing that cleavage of the signal peptide is mediated by signal peptidase II in both organisms. By using site-directed mutagenesis, the cysteine residue at the cleavage site was changed to glycine. Radiolabelled palmitate was not incorporated into the mutated protein, showing that lipid modification occurs at the Cys-22 residue.

7/7/8
DIALOG(R)File 5:Biosis Previews(R)

10230563 BIOSIS NO.: 199090015042
A LIPOPEPTIDE-ENCODING SEQUENCE UPSTREAM FROM THE LYS-A GENE OF PSEUDOMONAS-AERUGINOSA
AUTHOR: JANN A (Reprint); CAVARD D; MARTIN C; CAMI B; PATTE J-C
AUTHOR ADDRESS: LABORATOIRE CHIMIE BACTERIENNE, CNRS, 31 CHEMIN J AIGUIER, BP 71, MARSEILLE, FR**FRANCE
JOURNAL: Molecular Microbiology 4 (4): p677-682 1990
ISSN: 0950-382X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: An open reading frame (ORF) of 141 bp was observed upstream from the Pseudomonas aeruginosa lysA gene. The translation product of this ORF contains a signal peptide with a lipoprotein box, Ile-%%%Ala%%%-%%%Ala%%%-%%%Cys%%%, at the predicted signal peptidase cleavage site. The Escherichia coli phoA gene without its signal sequence was fused in frame to this ORF in a broad host-range plasmid. The resulting construct expressed a hybrid protein exhibiting alkaline phosphatase activity in phoA mutants of both E. coli and P. aeruginosa. This indicates that the ORF encodes a peptide, part of which acts as an export signal. The hybrid peptide was identified by immunoblotting with alkaline phosphatase antiserum. The accumulation of a precursor form was observed when P. aeruginosa cells carrying this gene fusion on a plasmid were treated with globomycin. Moreover, the mature form could be labelled with 2-[3H]-glycerol, indicating that lipidic residues may be linked to the hybrid protein. Taken together, these results strongly suggest that the ORF encodes a lipopeptide. We propose that the gene is called lppL.

7/7/9
DIALOG(R)File 5:Biosis Previews(R)

10194182 BIOSIS NO.: 199089112073
TRANSITION METAL COMPLEXES OF L CYSTEINE CONTAINING DIPEPTIDES AND TRIPEPTIDES
AUTHOR: CHERIFI K (Reprint); REVEREND B D-L; VARNAGY K; KISS T; SOVAGO I; LOUCHEUX C; KOZLOWSKI H
AUTHOR ADDRESS: INST CHEM, UNIV WROCLAW, 14 F JOLIOT-CURIE, 50-383 WROCLAW, POLAND**POLAND
JOURNAL: Journal of Inorganic Biochemistry 38 (1): p69-80 1990
ISSN: 0162-0134
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Nickel(II), cobalt(I), zinc(II), and cadmium(II) complexes of Ala-Cys, Phe-Cys, and %%%Ala%%%-%%%Ala%%%-%%%Cys%%% were studied by potentiometric and spectroscopic methods. Ni(II) induces deprotonation and coordination of the amide nitrogens, and the stable monomeric or oligomeric complexes are formed, depending on the metal to ligand molar ratios. Formation of the stable bis-complexes with { S,O } coordination mode is characteristic for cobalt(II), zinc(II), and cadmium(II) ions.

7/7/10
DIALOG(R)File 5:Biosis Previews(R)

09278288 BIOSIS NO.: 198886118209
AMINO ACID SEQUENCE OF A PROBABLE AMYLASE-PROTEASE INHIBITOR FROM RICE SEEDS
AUTHOR: YU Y G (Reprint); CHUNG C H; FOWLER A; SUH S W
AUTHOR ADDRESS: DEP CHEM, COLL NATURAL SCI, SEOUL NATL UNIV, SEOUL 141-742, KOREA**KOREA
JOURNAL: Archives of Biochemistry and Biophysics 265 (2): p466-475 1988
ISSN: 0003-9861
DOCUMENT TYPE: Article

RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The primary structure of a 9-kDa basic protein from rice seeds was determined by gas-phase sequencing of the intact protein and peptides derived from it by digestion with trypsin, chymotrypsin, and endopeptidase Lys-K. The protein consists of a single polypeptide chain of 91 amino acid residues with a calculated molecular mass of 8909 Da. It is rich in alanine, serine, glycine, and cysteine. The eight cysteines form four disulfide bonds. There is no methionine, histidine, phenylalanine, or tryptophan. The sequence is highly homologous with an .alpha.-amylase inhibitor, I-2, from seeds of Indian finger millet [F. A. P. Campos and M. Richardson (1984) FEBS Lett. 167, 221-225] and a 10-kDa barley seed protein, also called a probable amylase/protease inhibitor [B. Svensson et al. (1986) Carlsberg Res. Commun. 51, 493-500; J. Mundy and J. C. Rogers (1986) Planta 169, 51-63]. In analogy with the barley protein, the purified protein is tentatively called a rise probable amylase/protease inhibitor (PAPI). The rise PAPI does not show inhibitory activities against proteases and amylases tested. The amino acid sequence is as follows:
Ile-Thr-Cys-Gly-Gln-Val-Asn-Ser-Ala-Val-Gly-Pro-Cys-Leu-Thr-Tyr-Ala-Arg-Gly-Gly-Als-Gly-Pro-Ser-%%%Ala%%%-%%%Ala%%%-%%%Cys%%%
-Cys-Ser-Gly-Val-Arg-Ser-Leu-Lys-Ala-Ala-Ala-Ser-Thr-Thr-Ala-Asp-Arg-Arg-Thr-Ala-Cys-Asn-Cys-Leu-Lys-Asn-Ala-Ala-Arg-Gly-Ile-Lys-Gly-Leu-Asn-Ala-Gly-Asn-Ala-Ala-Ser-Ile-Pro-Ser-Lys-Cys-Gly-Val-Ser-Val-Pro-Tyr-Thr-Ile-Ser-Ala-Ser-Ile-Asp-Cys-Ser-Arg-Val-Ser.

7/7/11
DIALOG(R)File 5:Biosis Previews(R)

08674733 BIOSIS NO.: 198784028882
LIPOPROTEIN NATURE OF THE COLICIN A LYSIS PROTEIN EFFECT OF AMINO ACID SUBSTITUTIONS AT THE SITE OF MODIFICATION AND PROCESSING
AUTHOR: CAVARD D (Reprint); BATY D; HOWARD S P; VERHEIJ H M; LAZDUNSKI C
AUTHOR ADDRESS: CENT DE BIOCHIMIE ET BIOL MOLECULAIRE DU CENT NATIONAL DE LA RECHERCHE SCIENTIFIQUE, 13402 MARSEILLE CEDEX 9, FRANCE**FRANCE
JOURNAL: Journal of Bacteriology 169 (5): p2187-2194 1987
ISSN: 0021-9193
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The colicin A lysis protein (Cal) is required for the release of colicin A to the medium by producing bacteria. This protein is produced in a precursor form that contains a cysteine at the cleavage site (-Leu-%%%Ala%%%-%%%Ala%%%-%%%Cys%%%). The precursor must be modified by the addition of lipid before it can be processed. The maturation is prevented by globomycin, an inhibitor of signal peptidase II. Using oligonucleotide-directed mutagenesis, the alanine and cysteine residues in the -1 and +1 positions of the cleavage site were replaced by proline and threonine residues, respectively, in two different constructs. Both substitutions prevented the normal modification and cleavage of the protein. The marked activation of the outer membrane detergent-resistant phospholipase A observed with wild-type Cal was not observed with the Cal mutants. Both Cal mutants were also defective for the secretion of

colicin A. In one mutant, the signal peptide appeared to be cleaved off by an alternative pathway involving signal peptidase I. Electron microscope studies with immunogold labeling of colicin A on cryosections of pldA and cal mutant cells indicated that the colicin remains in the cytoplasm and is not transferred to the periplasmic space. These results demonstrate that Cal must be modified and processed to activate the detergent-resistant phospholipase A and to promote release of colicin A.

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DIALOG(R)File 5:Biosis Previews(R)

08617813 BIOSIS NO.: 198783096704
NUCLEOTIDE SEQUENCE OF THE GENE FOR THE PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN OF ESCHERICHIA-COLI K-12
AUTHOR: CHEN R (Reprint); HENNING U
AUTHOR ADDRESS: MAX-PLANCK-INST BIOLOGIE, CORRENSSTR 38, D-7400 TUEBINGEN, W GER**WEST GERMANY
JOURNAL: European Journal of Biochemistry 163 (1): p73-78 1987
ISSN: 0014-2956
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: During attempts to clone the gene for the Escherichia coli outer membrane protein III another gene was recovered. Its nucleotide sequence was determined and the deduced amino acid sequence showed that the gene does not encode protein III. It codes for a 173-residue polypeptide; 21 NH2-terminal residues are typical for a signal peptide. The sequence around the putative site (Ala-Cys) for removing this peptide, Ala-Ile-%%%Ala%%%-%%%Ala%%%-%%%Cys%%%-Ser-Ser-Asn, is highly homologous to that of the major cell envelope lipoprotein (Braun lipoprotein) surrounding its processing site; it is also homologous to the consensus pentapeptide Leu-Leu-Ala-Gly-Cys present in other lipoproteins of gram-negative bacteria. It could be shown that the gene expresses a lipoprotein with all the properties, including the amino acid composition, of the peptidoglycan-associated lipoprotein (PAL) [Mizuno, T. (1979) J. Biochem. (Tokyo) 86, 991-1000]. Therefore, the cloned gene is the pal gene. The protein does not contain hydrophobic regions which would serve as a membrane anchor. Tandemly repeated amino acid sequences exist at and near the NH2-terminus of the mature protein which are homologous to such repeats in the Braun lipoprotein, suggesting a common origin of this part of the two proteins. Attempts to place a transposon into the pal gene were unsuccessful. Hence the complete absence of the protein may be lethal and its function remains unknown.

7/7/13
DIALOG(R)File 5:Biosis Previews(R)

08614688 BIOSIS NO.: 198783093579
CHROMOPEPTIDES FROM PHYCOERYTHROCYANIN STRUCTURE AND LINKAGE OF THE THREE BILIN GROUPS
AUTHOR: BISHOP J E (Reprint); RAPOPORT H; KLOTZ A V; CHAN C F; GLAZER A N; FUGLISTALLER P; ZUBER H

AUTHOR ADDRESS: DEP OF CHEMISTRY, LAWRENCE BERKELEY LAB, UNIV OF CALIF, BERKELEY, CALIF 94720, USA**USA
JOURNAL: Journal of the American Chemical Society 109 (3): p875-881 1987
ISSN: 0002-7863
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Phycoerythrocyanin carries tow covalently attached phycocyanobilin (PCB) groups on the .beta. subunit and a phycobiliviolinoid (PXB) group on the .alpha. subunit. Three distinct bilipeptides were obtained by proteolytic digestion of this protein: Asn-Gln-%%%Ala%%%-%%%Ala%%%-%%%Cys%%%(PCB)-Ile-Arg, Gly-Asp-Cys(PCB)-Ser-Gln, and Cys(PXB)-Val-Arg. Correlative 500-MHz 1H NMR analyses showed that the heptapeptide and pentapeptide were attached by cysteinyl thioether linkage to the A ring of the PCB moiety. 1H NMR and mass spectrometry determinations led to structural assignment for the hitherto uncharacterized PXB moiety, with peptide-thioether bonding possible to either ring A or D. Amino acid sequence homologies strongly favor A-ring linkage.

08255116 BIOSIS NO.: 198682101503
PURIFICATION AND AMINO-TERMINAL SEQUENCE OF AN INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN SECRETED BY RAT LIVER BRL-3A CELLS
AUTHOR: MOTTOLA C (Reprint); MACDONALD R G; BRACKETT J L; MOLE J E; ANDERSON J K; CZECH M P
AUTHOR ADDRESS: DEP OF BIOCHEMISTRY, UNIV OF MASSACHUSETTS MED CENT, WORCESTER, MASSACHUSETTS 01605, USA**USA
JOURNAL: Journal of Biological Chemistry 261 (24): p11180-11188 1986
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A protein preparation that specifically binds insulin-like growth factors (IGFs) I and II was purified from medium conditioned by rat liver BRL-3A cells using molecular sieve chromatography in 1 M acetic acid followed by affinity chromatography on IGF-II-agarose. The affinity-purified IGF-binding protein exhibits a single major band with apparent Mr = 36,300 under reducing conditions on sodium dodecyl sulfate-polyacrylamide gels. The IGF-binding protein is efficiency and specifically cross-linked to either 125I-IGF-I (human) or 125I-IGF-II (rat) using disuccinimidyl suberate. An IGF-binding protein of similar apparent molecular weight was also affinity purified from rat hepatoma H-35 cell conditioned medium and found to differ from the BRL-3A protein such that potent polyclonal antisera prepared in rabbits against the purified BRL-3A IGF-binding protein exhibited a much lower titer for the H-35 protein in an enzyme-linked immunosorbent assay and upon immunoblotting. In order to determine whether a single BRL-3A IGF-binding protein is present in the affinity-purified preparation, the protein was prepared for sequencing on a Sephacryl S-300 column in 6 M guanidine HCl after reduction and alkylation. The amino acid composition (expressed in

percentages) of this IGF-binding protein was determined to be: Cys = 5.5, Lys = 4.8, His = 2.8, Arg = 7.8, Asx = 10.2, Thr = 5.1, Ser = 3.9, Glx = 15.7, Gly = 17.4, Ala = 7.3, Val = 4.6, Met = 1.4, Ile = 2.4, Leu = 8.3, Tyr = 1.0, Phe = 1.9. Sequencing of the NH2-terminal portion of this protien led to the idenification of 31 amino acids in the following order: Phe-Arg-Cys-Pro-Pro-Cys-Thr-Pro-Glu-Arg-Leu-%%%Ala%%%-%%%Ala%%%-%%%Cys%%%
-Gly-Pro-Pro-Pro-Asp-Ala-Pro-Cys-Ala-Glu-Leu-Val-Arg-Glu-Pro-Gly-Cys. We conclude that rat liver BRL-3A cells secrete a single major IGF-binding protein capable of binding both IGF-I and IGF-II.

7/7/15
DIALOG(R)File 5:Biosis Previews(R)

08170978 BIOSIS NO.: 198682017365
THE AMINO-ACID SEQUENCE OF THE NONSPECIFIC LIPID TRANSFER PROTEIN FROM GERMINATED CASTOR-BEAN ENDOSPERMS
AUTHOR: TAKISHIMA K (Reprint); WATANABE S; YAMADA M; MAMIYA G
AUTHOR ADDRESS: DEP OF BIOL, UNIV OF TOKYO, KOMABA, MEGURO, TOKYO 153, JAPAN**JAPAN
JOURNAL: Biochimica et Biophysica Acta 870 (2): p248-255 1986
ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The amino-acid sequence of the nonspecific lipid-transfer protein from germinated castor bean endosperms has been determined by automatic sequencing of Staphylococcus aureus proteinase and tryptic peptides. The protein has 92 residues and a molecular weight of 9313. The complete primary structure of this protein is:
Val-Asp-Cys-Gly-Gln-Val-Asn-Ser-Ser-Leu10-Ala-Ser-Cys-Ile-Pro-Phe-Leu-Thr-Gly-Gly20-Val-Ala-Ser-Pro-Ser-Ala-Ser-Cys-Cys-Ala30-Gly-Val-Gln-Asn-Leu-Lys-Thr-Leu-Ala-Pro40-Thr-Ser-Ala-Asp-Arg-Arg-%%%Ala%%%-%%%Ala%%%-%%%Cys%%%
-Glu50-Cys-Ile-Lys-Ala-Ala-Ala-Ala-Arg-Phe-Pro60-Thr-Ile-Lys-Gln-Asp-Ala-Ala-Ser-Ser-Leu70-Pro-Lys-Lys-Cys-Gly-Val-Asp-Ile-Asn-Ile80-Pro-Ile-Ser-Lys-Thr-Thr-Asn-Cys-Gln-Ala90-Ile-Asn. Sequence microheterogeneity was found at residues 42 and 50, suggesting the occurrence of two genes for this protein or the allelic variation of the same gene. 12 to 14 acidic and basic amino acids were located on the latter half of the sequence. The first 20 residues of this protein have a homology (45%) with the residues 2-21 of the lipid-transfer protein from spinach leaf.

7/7/16
DIALOG(R)File 5:Biosis Previews(R)

08067079 BIOSIS NO.: 198681030970
SUBTILISIN A A NEW ANTIBIOTIC PEPTIDE PRODUCED BY BACILLUS-SUBTILIS 168 ISOLATION STRUCTURAL ANALYSIS AND BIOGENESIS
AUTHOR: BABASAKI K (Reprint); TAKAO T; SHIMONISHI Y; KURAHASHI K
AUTHOR ADDRESS: INST PROTEIN RES, OSAKA UNIV, YAMADAOKA, SUITA, OSAKA 565** JAPAN

JOURNAL: Journal of Biochemistry (Tokyo) 98 (3): p585-604 1985
ISSN: 0021-924X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Subtilosin A, a new antibiotic produced by Bacillus subtilis 168, was extracted from culture medium with n-butanol and purified to homogeneity by a combination of gel filtration and thin-layer chromatography. The yield was 5.5 mg from a liter of culture. It had bacteriocidal activity against some gram-positive bacteria. Amino acid analysis and mass spectrometry showed that it was a peptide with a molecular weight of 3398.9, consisting of 32 usual amino acid and some non-amino acid residues. Its amino- and carboxyl-termini were blocked. By analysis of the fragments obtained by partial acid hydrolysis, as well as by chymotryptic and thermolysin digestions of reduced and S-carboxymethylated samples and Achromobacter protease I digestion of performic acid-oxidized samples, the amino acid sequence was determined to be as follows:
X-Gly-Leu-Gly-Leu-Trp-Gly-Asn-Lys-Gly-Cys-Ala-Thr-Cys-Ser-Ile-Gly-%%%Ala%%%-%%%Ala%%%-%%%Cys%%%
-Leu-Val-Asp-Gly-Pro-Ile-Pro-Asp-Glx-Ile-Ala-Gly-Ala. The analyses of cross-linking structures revealed that there were linkages between the amino- and carboxyl-termini and between the Cys-19 and the Glx-28 residues through an unknown residue with a residue weight of 163. Consequently, subtilosin A was deduced to be a cyclic peptide antibiotic with a novel cross-linking structure. The production of subtilosin A begins at the end of vegetative growth and finishes before spore formation. Studies on the correlation between the production of subtilosin A and spore formation with decoyinine in the original strain and in asporogenous mutants of B. subtilis 168 suggested that there was no close correlation between the two phenomena. The production of subtilosin A was repressed by inhibitors of protein and RNA synthesis in contrast to that of many other antibiotic peptides, suggesting that it is synthesized by the mechanism of usual protein synthesis.

07588228 BIOSIS NO.: 198579007127
CHEMICAL SIMULATION OF RUBREDOXIN BY IRON-II-TETRAPEPTIDE COMPLEXES IN AQUEOUS TRITON X-100 MICELLE SOLUTION
AUTHOR: NAKATA M (Reprint); UEYAMA N; FUJI M-A; NAKAMURA A; WADA K; MATSUBARA H
AUTHOR ADDRESS: DEP MACROMOLECULAR SCIENCE, FAC SCIENCE, OSAKA UNIV, TOYONAKA, OSAKA 560, JAPAN**JAPAN
JOURNAL: Biochimica et Biophysica Acta 788 (3): p306-312 1984
ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The Fe(II) complexes of the type Fe(L-L)2 (L = anion of Z-Cys-Thr-Val-Cys-OMe, Z-Cys-Pro-Leu-Cys-OMe, Z-%%%Cys%%%-%%%Ala%%%-%%%Ala%%%-%%%Cys%%%-OMe, or Z-Ala-Cys-OMe (Z = benzyloxycarbonyl)) were

synthesized in aqueous 10% Triton X-100 solution and were characterized by the absorption, CD [circular dichroism] and MCD [magnetic circular dichroism] spectra. The spectra indicated a core structure similar to that of native rubredoxin [from Clostridium pasteurianum]. Among the complexes, only the Fe(II) complex of Z-Cys-Pro-Leu-Cys-OMe provides a quasi-reversible redox couple at -0.37 V vs. standard calomel electrolyte in aqueous Triton X solution (-0.30 V vs. standard calomel electrode for native rubredoxin in aqueous solution). The Fe(II) complex of Z-Cys-Pro-Leu-Cys-OMe exhibits a remarkable electron-transfer activity in the system of NADPH/ferredoxin:NADP+ oxidoreductase/FeII peptide complex/ferricytochrome c.

7/7/18
DIALOG(R)File 5:Biosis Previews(R)

07343351 BIOSIS NO.: 198478078758
BILIN ATTACHMENT SITES IN THE ALPHA SUBUNIT AND BETA SUBUNIT OF B PHYCOERYTHRIN STRUCTURAL STUDIES ON THE SINGLY LINKED PHYCO ERYTHRO BILINS
AUTHOR: SCHOENLEBER R W (Reprint); LUNDELL D J; GLAZER A N; RAPOPORT H
AUTHOR ADDRESS: DEP CHEMISTRY, UNIV CALIF, BERKELEY, CA 94720, USA**USA
JOURNAL: Journal of Biological Chemistry 259 (9): p5485-5489 1984
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Five unique phycoerythrobilin (PEB) peptides were prepared from Porphyridium cruentum B-phycoerythrin by a combination of tryptic and thermolytic digestion without alteration in the spectroscopic properties of the bilin: .alpha.-1 Cys(PEB)-Tyr-Arg; .alpha.-2 Leu-Cys(PEB)-Val-Pro-Arg; .beta.-1 Met-%%%Ala%%%-%%%Ala%%%-%%%Cys%%% (PEB)-Leu-Arg; .beta.-2T Phe-Ala-Ala-Gly-Asp-Cys(PeB)-Thr-Ser; .beta.-3T .**GRAPHIC**. where .alpha. and .beta. refer to the subunits from which the peptides were derived. High resolution 1H NMR analysis of peptides .alpha.-2, .beta.-1, and .beta.-2T combined with earlier studies of peptide .alpha.-1 provided proof that all of the singly linked PEB peptides contain a thioether bond to the 3' position of ring A, and strong evidence in support of a trans-dihydro ring A in each of these chromopeptides. The circular dichroism spectra of the 4 singly linked PEB peptides show that the configuration at C-16 is R in each instance. The present study coupled with previously reported results on peptide .beta.-3T provides the 1st comprehensive analysis of the structure of all the polypeptide-linked prosthetic groups on the .alpha. and .beta. subunits of B-phycoerythrin.

7/7/19
DIALOG(R)File 5:Biosis Previews(R)

07343350 BIOSIS NO.: 198478078757
BILIN ATTACHMENT SITES IN THE ALPHA SUBUNIT AND BETA SUBUNIT OF B PHYCOERYTHRIN AMINO-ACID SEQUENCE STUDIES
AUTHOR: LUNDELL D J (Reprint); GLAZER A N; DELANGE R J; BROWN D M

AUTHOR ADDRESS: DEP MICROBIOL IMMUNOL, UNIV CALIF, BERKELEY, CA 94720, USA **USA
JOURNAL: Journal of Biological Chemistry 259 (9): p5472-5480 1984
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The amino acid sequence about the sites of attachment of all of the bilin prosthetic groups of the .alpha. and .beta. subunits of Porphyridium cruentum B-phycoerythrin was determined. The sequences of 5 unique tryptic peptides, each carrying one phycoerythrobilin, are as follows: .alpha.-1 Ile-Asx-Lys-Cys*-Tyr-Arg; .alpha.-2 Asx-Arg-Leu-Cys*-Val-Pro-Arg; .beta.-1 Met-%%%Ala%%%-%%%Ala%%%-%%%Cys%%% *-Leu-Arg; .beta.-2 Met-Ser-Phe-Ala-Ala-Gly-Asp-Cys*-Thr-Ser-Leu-Ala-Ser-Glu-Val-Ala-Gln-Tyr-Phe-Asp-Arg; .beta.-3 Leu-Asp-Ala-Val-Asn-Ser-Ile-Val-Ser-Asn-Ala-Ser-Cys*-Met-Val-Ser-Asp-Ala-Val-Ser-Gly-Met-Ile-Cys*-Glu-Asn-Pro-Gly-Leu-Ile-Ser-Pro-Gly-Gly-Asn-Cys-Tyr-Thr-Asn-Arg; where the designations .alpha. and .beta. refer to the subunit from which the peptide was derived. (Cysteinyl residues involved in bilin attachment are indicated with an asterisk). The bilins in peptides .alpha.-1, .alpha.-2, .beta.-1, and .beta.-2 are attached to the peptide through a single thioether linkage to a cysteinyl residue. In contrast, the phycoerythrobilin on peptide .beta.-3 is attached through 2 thioether linkages to cysteinyl residues 10 residues apart. This appears to be the 1st report of a prosthetic group covalently bound to a polypeptide through 2 linkages separated by such a considerable distance in the linear sequence. The visible absorption spectrum of peptide .beta.-3 is red-shifted by about 10 nm relative to the spectra of the other 4 bilin peptides. Comparison of the sequences from B-phycoerythrin to sequences of several other biliproteins revealed the presence of a number of invariant tyrosyl and arginyl residues near bilin attachment sites.

7/7/20
DIALOG(R)File 5:Biosis Previews(R)

05421546 BIOSIS NO.: 197866008030
THE SULFHYDRYL GROUPS INVOLVED IN THE ACTIVE SITE OF MYOSIN B ATPASE PART 4 STRUCTURE AROUND THE S-A THIOL GROUP
AUTHOR: HORIGOME T (Reprint); YAMASHITA T
AUTHOR ADDRESS: LAB PHYSIOL CHEM, SCH MED, JUNTENDO UNIV, BUNKYO, TOKYO 113, JPN**JAPAN
JOURNAL: Journal of Biochemistry (Tokyo) 83 (1): p49-56 1978
ISSN: 0021-924X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The structure of a tryptic peptide containing 1 specific sulfhydryl group (Sa), which is responsible for the activation of Mg2+-ATPase of [rabbit skeletal muscle] myosin B and is present in the light meromyosin region of the myosin molecule, was studied. The amino acid sequence was deduced to be Thr (or Ser)-Asn-%%%Ala%%%-%%%Ala%%%-

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  %%%Cys%%%-Ala-Ala-Leu-Asp-Lys-Lys. A space-filling model around Sa was
  built up by comparing Sa-peptide with the amino acid sequence around Cys
  190 of .alpha.-tropomyosin, and the high reactivity of Sa with
  N-ethylmaleimide is considered based on this model.
? s s7 and heme
              20  S7
           31721  HEME
      S8       0  S7 AND HEME
? s s7 and haem
              20  S7
            2724  HAEM
      S9       0  S7 AND HAEM
? ds

Set     Items   Description
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S2          0   ((HEME OR HAEM)()?PEPTIDE)
S3        104   ((HEME OR HAEM)()PEPTIDE)
S4          6   S3 AND CYSTEINE
S5          0   S3 AND (C-X-X-C)
S6          0   S3 AND (CYS()ALA()ALA()CYS)
S7         20   (CYS()ALA()ALA()CYS)
S8          0   S7 AND HEME
S9          0   S7 AND HAEM
? s s3 and s7
             104  S3
              20  S7
     S10       0  S3 AND S7
? ds
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   $315.62  Estimated cost File5
     $2.93  TELNET
   $318.55  Estimated cost this search
   $318.55  Estimated total session cost   3.146 DialUnits
Logoff: level 05.17.01 D  10:27:26
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File 5:Biosis Previews(R) 1926-2007/Jun W3
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           13327  C6
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            3217  CNBR
             135  S1
      S2       0  CNBR AND S1
? s (heme()peptide) and s1
           31721  HEME
          292391  PEPTIDE
             102  HEME(W)PEPTIDE
             135  S1
      S3       0  (HEME()PEPTIDE) AND S1
? s s1 and heme
             135  S1
           31721  HEME
      S4      40  S1 AND HEME
? s s1 and (Cys()Ala()Ala()Cys)
             135  S1
           15333  CYS
           28026  ALA
           28026  ALA
           15333  CYS
               8  CYS(W)ALA(W)ALA(W)CYS
      S5       0  S1 AND (CYS()ALA()ALA()CYS)
? t s4/7/1-40

 4/7/1
DIALOG(R)File 5:Biosis Previews(R)
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0019590435  BIOSIS NO.: 200700250176
Convergent evolution of cytochrome c(6) and plastocyanin - The evolutionary
  pathways of the two proteins are connected to the geochemical changes in
  iron and copper availabilities
BOOK TITLE: Advances in Photosynthesis and Respiration:THE LIGHT-DRIVEN
  PLASTOCYANIN: FERREDOXIN OXIDOREDUCTASE
AUTHOR: De la Rosa Miguel A (Reprint); Molina-Heredia Fernando P; Hervas
  Manuel; Navarro Jose A
BOOK AUTHOR/EDITOR: Golbeck JH (Editor)
AUTHOR ADDRESS: Univ Seville, Inst Bioquim Vegetal and Fotosintesis,
  Americo Vespucio 49, Seville 41092, Spain**Spain
AUTHOR E-MAIL ADDRESS: marosa@us.es
SERIES TITLE: ADVANCES IN PHOTOSYNTHESIS AND RESPIRATION  24 p683-696,CP16
2006
BOOK PUBLISHER: SPRINGER, PO BOX 17, 3300 AA DORDRECHT, NETHERLANDS
ISBN: 978-1-4020-4255-3 (H)
DOCUMENT TYPE: Book Chapter
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RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Cytochrome c(6) and plastocyanin are an excellent case study of the convergent evolution of proteins. The two molecules differ in their primary sequence and 3D structure but function in a similar way to transfer electrons from cytochrome b(6) f to Photosystem I. lt seems that cytochrome c(6) was first "discovered" by Nature when iron was much more available than copper because of the reducing character of the Earth's atmosphere. As the atmospheric molecular oxygen concentration began to rise because of photosynthetic activity, the relative bioavailabilities of iron and copper declined and rose, respectively, and cytochrome c(6) was replaced with plastocyanin. Such a transition from the %%%heme%%% protein to the copper protein would have indeed involved an evolution of the reaction mechanism, as inferred from the comparative analysis of the structure-function relationships of plastocyanin and cytochrome c(6) isolated from a number of differently evolved organisms. Three different kinetic models for the reaction mechanism have been proposed: type I (an oriented collisional model), type II (a minimal two-step mechanism involving formation of a transient complex), and type III (a mechanism requiring an additional rearrangement step to make the redox centers orientate properly within the complex). The mechanism of heuristic searching in molecular recognition is thus a product of evolution rather than an inherent feature of molecular interactions. In plants, cytochrome c(6) is not produced as such but there exists a cytochrome c(6)-like protein (herein called cytochrome cp) that could be phyllogenetically related to cyanobacterial cytochrome cm.

4/7/2
DIALOG(R)File 5:Biosis Previews(R)

19369019 BIOSIS NO.: 200700028760
Identification of precise electrostatic recognition sites between cytochrome c(6) and the photosystem I subunit PsaF using mass spectrometry
AUTHOR: Sommer Frederik; Drepper Friedel; Haehnel Wolfgang; Hippler Michael (Reprint)
AUTHOR ADDRESS: Univ Munster, Inst Plant Biochem and Biotechnol, Dept Biol, Hindenburgpl 55, D-48143 Munster, Germany**Germany
AUTHOR E-MAIL ADDRESS: mhippler@uni-muenster.de
JOURNAL: Journal of Biological Chemistry 281 (46): p35097-35103 NOV 17 2006 2006
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The reduction of the photo-oxidized special chlorophyll pair P700 of photosystem I (PSI) in the photosynthetic electron transport chain of eukaryotic organisms is facilitated by the soluble copper-containing protein plastocyanin (pc). In the absence of copper, pc is functionally replaced by the %%%heme%%%-containing protein cytochrome c(6) (cyt c(6)) in the green alga Chlamydomonas reinhardtii. Binding and electron transfer between both donors and PSI follows a two-step mechanism that depends on electrostatic and hydrophobic recognition between the

partners. Although the electrostatic and hydrophobic recognition sites on pc and PSI are well known, the precise electrostatic recognition site on cyt c(6) is unknown. To specify the interaction sites on a molecular level, we cross-linked cyt c(6) and PSI using a zero-length cross-linker and obtained a cross-linked complex competent in fast and efficient electron transfer. As shown previously, cyt c(6) cross-links specifically with the PsaF subunit of PSI. Mass spectrometric analysis of tryptic peptides from the cross-linked product revealed specific interaction sites between residues Lys(27) of PsaF and Glu(69) of cyt c(6) and between Lys(23) of PsaF and Glu(69)/Glu(70) of cyt c(6). Using these new data, we present a molecular model of the intermolecular electron transfer complex between eukaryotic cyt c(6) and PSI.

4/7/3
DIALOG(R)File 5:Biosis Previews(R)

19207580 BIOSIS NO.: 200600552975
A brownian dynamics study of the interactions of the luminal domains of the cytochrome b(6)f complex with plastocyanin and cytochrome c(6): The effects of the Rieske FeS protein on the interactions
AUTHOR: Haddadian Esmael J; Gross Elizabeth L (Reprint)
AUTHOR ADDRESS: Ohio State Univ, Dept Biochem, Columbus, OH 43210 USA**USA
AUTHOR E-MAIL ADDRESS: gross.3@osu.edu
JOURNAL: Biophysical Journal 91 (7): p2589-2600 OCT 2006 2006
ISSN: 0006-3495
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The availability of the structures of the cytochrome b(6)f complex (cyt b(6)f), plastocyanin (PC), and cytochrome c(6) (cyt c(6)) from Chlamydomonas reinhardtii allowed us, for the first time, to model electron transfer interactions between the luminal domains of this complex (including cyt f and the Rieske FeS protein) and its redox partners in the same species. We also generated a model structure in which the FeS center of the Rieske protein was positioned closer to the %%%heme%%% of cyt f than observed in the crystal structure and studied its interactions with both PC and cyt c(6). Our data showed that the Rieske protein in both the original crystal structure and in our modeled structure of the cyt b(6)f complex did not physically interfere with binding position or orientation of PC or cyt c(6) on cyt f. PC docked on cyt f with the same orientation in the presence or the absence of the Rieske protein, which matched well with the previously reported NMR structures of complexes between cyt f and PC. When the FeS center of the Rieske protein was moved close to the %%%heme%%% of cyt f, it even enhanced the interaction rates. Studies using a cyt f modified in the 184-191 loop showed that the cyt f structure is a more important factor in determining the rate of complex formations than is the presence or the absence of the Rieske protein or its position with respect to cyt f.

4/7/4
DIALOG(R)File 5:Biosis Previews(R)

19122218 BIOSIS NO.: 200600467613
Detecting transient protein-protein interactions by X-ray absorption spectroscopy: The cytochrome c(6)-photosystem I complex
AUTHOR: Diaz-Moreno Irene; Diaz-Quintana Antonio; Subias Gloria; Mairs Trevor; De la Rosa Miguel A (Reprint); Diaz-Moreno Sofia
AUTHOR ADDRESS: Univ Sevilla, Inst Bioquim Vegetal and Fotosintesis, Americo Vespucio 49, Seville 41092, Spain**Spain
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JOURNAL: FEBS Letters 580 (13): p3023-3028 MAY 29 2006 2006
ISSN: 0014-5793
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Reliable analysis of the functionality of metalloproteins demands a highly accurate description of both the redox state and geometry of the metal centre, not only in the isolated metalloprotein but also in the transient complex with its target. Here, we demonstrate that the transient interaction between soluble cytochrome c(6) and membrane-embedded photosystem I involves subtle changes in the %%%heme%%% iron, as inferred by X-ray absorption spectroscopy (XAS). A slight shift to lower energies of the absorption edge of Fe2+ in cytochrome c(6) is observed upon interaction with photosystem I. This work constitutes a novel application of XAS to the analysis of weak complexes in solution.

4/7/5

18307355 BIOSIS NO.: 200510001855
Brownian dynamics study of cytochrome f interactions with cytochrome c(6) and plastocyanin in Chlamydomonas reinhardtii plastocyanin, and cytochrome c(6) mutants
AUTHOR: Haddadian Esmael J; Gross Elizabeth L (Reprint)
AUTHOR ADDRESS: Ohio State Univ, Dept Biochem, 484 W 12th Ave, Columbus, OH 43210 USA**USA
AUTHOR E-MAIL ADDRESS: gross.3@osu.edu
JOURNAL: Biophysical Journal 88 (3): p2323-2339 MAR 05 2005
ISSN: 0006-3495
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Using Brownian dynamics simulations, all of the charged residues in Chlamydomonas reinhardtii cytochrome c(6) (cyt c6) and plastocyanin (PC) were mutated to alanine and their interactions with cytochrome f (cyt f) were modeled. Systematic mutation of charged residues on both PC and cyt c(6) confirmed that electrostatic interactions (at least in vitro) play an important role in bringing these proteins sufficiently close to cyt f to allow hydrophobic and van der Waals interactions to form the final electron transfer-active complex. The charged residue mutants on PC and cyt c6 displayed similar inhibition classes. Our results indicate a difference between the two acidic clusters on PC. Mutations D44A and E43A of the lower cluster showed greater inhibition

than do any of the mutations of the upper cluster residues. Replacement of acidic residues on cyt c6 that correspond to the PC's lower cluster, particularly E70 and E69, was observed to be more inhibitory than those corresponding to the upper cluster. In PC residues D42, E43, D44, D53, D59, D61, and E85, and in cyt c(6) residues D2, E54, K57, D65, R66, E70, E71, and the %%%heme%%% had significant electrostatic contacts with cyt f charged residues. PC and cyt c(6) showed different binding sites and orientations on cyt f. As there are no experimental cyt c(6) mutation data available for algae, our results could serve as a good guide for future experimental work on this protein. The comparison between computational values and the available experimental data (for PC-cyt f interactions) showed overall good agreement, which supports the predictive power of Brownian dynamics simulations in mutagenesis studies.

4/7/6
DIALOG(R)File 5:Biosis Previews(R)

18170215 BIOSIS NO.: 200500077280
Genetic dissection of nutritional copper signaling in chlamydomonas distinguishes regulatory and target genes
AUTHOR: Eriksson Mats; Moseley Jeffrey L (Reprint); Tottey Stephen; Del Campo Jose A; Quinn Jeanette; Kim Youngbae; Merchant Sabeeha
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JOURNAL: Genetics 168 (2): p795-807 October 2004 2004
MEDIUM: print
ISSN: 0016-6731 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A genetic screen for Chlamgdomonas reinhardtii mutants with copper-dependent growth or nonphotosynthetic phenotypes revealed three loci, COPPER RESPONSE REGULATOR 1 (CRR1), COPPER RESPONSE DEFECT 1 (CRD1), and COPPER RESPONSE DEFECT 2 (CRD2), distinguished as regulatory or target genes on the basis of phenotype. CRR1 was shown previously to be required for transcriptional activation of target genes like CYC6, CPX1, and CRD1, encoding, respectively, %%%cytochrome%%% %%%c6%%% (which is a %%%heme%%%-containing substitute for copper-containing plastocyanin), coproporphyrinogen III oxidase, and Mg-protoporphyrin IX monomethylester cyclase. We show here that CRR1 is required also for normal accumulation of copper proteins like plastocyanin and ferroxidase in copper-replete medium and for apoplastocyanin degradation in copper-deficient medium, indicating that a single pathway controls nutritional copper homeostasis at multiple levels. CPR1 is linked to the SUPPRESSOR of PCY1-AC208 13 (SOP13) locus, which corresponds to a gain-of-function mutation resulting in copper-independent expression of CYC6 CRR1 is required also for hypoxic growth, pointing to a physiologically meaningful regulatory connection between copper deficiency and hypoxia. The growth phenotype of crr1 strains results primarily from secondary iron deficiency owing to reduced ferroxidase abundance, suggesting a role for CRR1 in copper distribution to a multicopper ferroxidase involved in iron assimilation. Mutations at the CRD2 locus also result in copper-conditional iron deficiency, which is

consistent with a function for CRD2 in a pathway for copper delivery to the ferroxidase. Taken together, the observations argue for a specialized copper-deficiency adaptation for iron uptake in Chlamydomonas.

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DIALOG(R)File 5:Biosis Previews(R)

17850666 BIOSIS NO.: 200400220721
The efficient functioning of photosynthesis and respiration in Synechocystis sp. PCC 6803 strictly requires the presence of either %%%cytochrome%%% %%%c6%%% or plastocyanin.
AUTHOR: Duran Raul V; Hervas Manuel; De la Rosa Miguel A (Reprint); Navarro Jose A
AUTHOR ADDRESS: Instituto de Bioquimica Vegetal y Fotosintesis, Universidad de Sevilla y Consejo Superior de Investigaciones Cientificas, Americo Vespucio s/n, 41092, Sevilla, Spain**Spain
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JOURNAL: Journal of Biological Chemistry 279 (8): p7229-7233 February 20, 2004 2004
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: In cyanobacteria, %%%cytochrome%%% %%%c6%%% and plastocyanin are able to replace each other as redox carriers in the photosynthetic and respiratory electron transport chains with the synthesis of one or another protein being regulated by the copper concentration in the culture medium. However, the presence of a third unidentified electron carrier has been suggested. To address this point, we have constructed two deletion mutants of the cyanobacterium Synechocystis sp. PCC 6803, each variant lacking either the petE or petJ gene, which respectively codes for the copper or %%%heme%%% protein. The photoautotrophic and heterotrophic growth rate of the two mutants in copper-free and copper-supplemented medium as well as their photosystem I reduction kinetics in vivo were compared with those of wild-type cells. The two mutant strains grow at equivalent rates and show similar in vivo photosystem I reduction kinetics as wild-type cells when cultured in media that allow the expression of just one of the two electron donor proteins, but their ability to grow and reduce photosystem I is much lower when neither %%%cytochrome%%% %%%c6%%% nor plastocyanin is expressed. These findings indicate that the normal functioning of the cyanobacterial photosynthetic and respiratory chains obligatorily depends on the presence of either %%%cytochrome%%% %%%c6%%% or plastocyanin.

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DIALOG(R)File 5:Biosis Previews(R)

17643693 BIOSIS NO.: 200400010677
Metalloprotein association, self-association, and dynamics governed by hydrophobic interactions: Simultaneous occurrence of gated and true electron-transfer reactions between cytochrome f and %%%cytochrome%%%

%%%c6%%% from Chlamydomonas reinhardtii.
AUTHOR: Grove Tijana Z; Kostic Nenad M (Reprint)
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JOURNAL: Journal of the American Chemical Society 125 (35): p10598-10607 September 3, 2003 2003
MEDIUM: print
ISSN: 0002-7863 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Noninvasive reconstitution of the %%%heme%%% in %%%cytochrome%%% %%%c6%%% with zinc(II) ions allowed us to study the photoinduced electron-transfer reaction 3Zncyt c6+cyt f(III)fwdarwZncyt c6++cyt f(II) between physiological partners %%%cytochrome%%% %%%c6%%% and cytochrome f, both from Chlamydomonas reinhardtii. The reaction kinetics was analyzed in terms of protein docking and electron transfer. In contrast to various protein pairs studied before, both the unimolecular and the bimolecular reactions of this oxidative quenching take place at all ionic strengths from 2.5 through 700 mM. The respective intracomplex rate constants are kuni (1.2+-0.1)X104 s-1 for persistent and kbi (9+-4)X102 s-1 for the transient protein complex. The former reaction seems to be true electron transfer, and the latter seems to be electron transfer gated by a structural rearrangement. Remarkably, these reactions occur simultaneously, and both rate constants are invariant with ionic strength. The association constant Ka for zinc %%%cytochrome%%% %%%c6%%% and cytochrome f(III) remains (5+-3)X105 M-1 in the ionic strength range from 700 to 10 mM and then rises slightly to (7+-2)X106 M-1, as ionic strength is lowered to 2.5 mM. Evidently, docking of these proteins from C. reinhardtii is due to hydrophobic interaction, slightly augmented by weak electrostatic attraction. Kinetics, chromatography, and cross-linking consistently show that cytochrome f self-dimerizes at ionic strengths of 200 mM and higher. Cytochrome f(III) quenches triplet state 3Zncyt c6, but its dimer does not. Formation of this unreactive dimer is an important step in the mechanism of electron transfer. Not only association between the reacting proteins, but also their self-association, should be considered when analyzing reaction mechanisms.

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DIALOG(R)File 5:Biosis Previews(R)

17480277 BIOSIS NO.: 200300437311
Brownian dynamics simulations of the interaction of Chlamydomonas cytochrome f with plastocyanin and %%%cytochrome%%% %%%c6%%%.
AUTHOR: Gross Elizabeth L (Reprint); Pearson Douglas C
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JOURNAL: Biophysical Journal 85 (3): p2055-2068 September 2003 2003
MEDIUM: print
ISSN: 0006-3495 _(ISSN print)
DOCUMENT TYPE: Article

RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The interaction of Chlamydomonas cytochrome f (cyt f) with either Chlamydomonas plastocyanin (PC) or Chlamydomonas %%%cytochrome%%% %%%c6%%% (cyt c6) was studied using Brownian dynamics simulations. The two electron acceptors (PC and cyt c6) were found to be essentially interchangeable despite a lack of sequence homology and different secondary structures (beta-sheet for PC and alpha-helix for cyt c6). Simulations using PC and cyt c6 interacting with cyt f showed approximately equal numbers of successful complexes and calculated rates of electron transfer. Cyt f-PC and cyt f-cyt c6 showed the same types of interactions. Hydrophobic residues surrounding the Y1 ligand to the %%%heme%%% on cyt f interacted with hydrophobic residues on PC (surrounding the H87 ligand to the Cu) or cyt c6 (surrounding the %%%heme%%%). Both types of complexes were stabilized by electrostatic interactions between K65, K188, and K189 on cyt f and conserved anionic residues on PC (E43, D44, D53, and E85) or cyt c6 (E2, E70, and E71). Mutations on cyt f had identical effects on its interaction with either PC or cyt c6. K65A, K188A, and K189A showed the largest effects whereas residues such as K217A, R88A, and K110A, which are located far from the positive patch on cyt f, showed very little inhibition. The effect of mutations observed in Brownian dynamics simulations paralleled those observed in experiments.

17302878 BIOSIS NO.: 200300261522
A comparative structural and functional analysis of cyanobacterial plastocyanin and %%%cytochrome%%% %%%c6%%% as alternative electron donors to Photosystem I. Photosystem I reduction in cyanobacteria.
AUTHOR: Diaz-Quintana Antonio; Navarro Jose A; Hervas Manuel; Molina-Heredia Fernando P; De la Cerda Berta; De la Rosa Miguel A (Reprint)
AUTHOR ADDRESS: Instituto de Bioquimica Vegetal y Fotosintesis, Universidad de Sevilla y Consejo Superior de Investigaciones Cientificas, Americo Vespucio s/n, Centro Isla de la Cartuja, 41092, Sevilla, Spain**Spain
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JOURNAL: Photosynthesis Research 75 (2): p97-110 2003 2003
MEDIUM: print
ISSN: 0166-8595 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Plastocyanin and %%%cytochrome%%% %%%c6%%% are two soluble metalloproteins that act as alternative electron carriers between the membrane-embedded complexes cytochromes b6f and Photosystem I. Despite plastocyanin and %%%cytochrome%%% %%%c6%%% differing in the nature of their redox center (one is a copper protein, the other is a %%%heme%%% protein) and folding pattern (one is a beta-barrel, the other consists of alpha-helices), they are exchangeable in green algae and cyanobacteria. In fact, the two proteins share a number of structural similarities that allow them to interact with the same membrane complexes in a similar way.

The kinetic and thermodynamic analysis of Photosystem I reduction by plastocyanin and %%%cytochrome%%% %%%c6%%% reveals that the same factors govern the reaction mechanism within the same organism, but differ from one another. In cyanobacteria, in particular, the electrostatic and hydrophobic interactions between Photosystem I and its electron donors have been analyzed using the wild-type protein species and site-directed mutants. A number of residues similarly conserved in the two proteins have been shown to be critical for the electron transfer reaction. %%%Cytochrome%%% %%%c6%%% does contain two functional areas that are equivalent to those previously described in plastocyanin: one is a hydrophobic patch for electron transfer (site 1), and the other is an electrically charged area for complex formation (site 2). Each cyanobacterial protein contains just one arginyl residue, similarly located between sites 1 and 2, that is essential for the redox interaction with Photosystem I.

17111442 BIOSIS NO.: 200300070161
The interactions of cyanobacterial %%%cytochrome%%% %%%c6%%% and cytochrome f, characterized by NMR.
AUTHOR: Crowley Peter B; Diaz-Quintana Antonio; Molina-Heredia Fernando P; Nieto Pedro; Sutter Martin; Haehnel Wolfgang; De la Rosa Miguel A; Ubbink Marcellus (Reprint)
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JOURNAL: Journal of Biological Chemistry 277 (50): p48685-48689 December 13, 2002 2002
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: During oxygenic photosynthesis, %%%cytochrome%%% %%%c6%%% shuttles electrons between the membrane-bound complexes cytochrome bf and photosystem I. Complex formation between Phormidium laminosum cytochrome f and %%%cytochrome%%% %%%c6%%% from both Anabaena sp. PCC 7119 and Synechococcus elongatus has been investigated by nuclear magnetic resonance spectroscopy. Chemical-shift perturbation analysis reveals a binding site on Anabaena %%%cytochrome%%% %%%c6%%%, which consists of a predominantly hydrophobic patch surrounding the %%%heme%%% substituent, methyl 5. This region of the protein was implicated previously in the formation of the reactive complex with photosytem I. In contrast to the results obtained for Anabaena %%%cytochrome%%% %%%c6%%%, there is no evidence for specific complex formation with the acidic %%%cytochrome%%% %%%c6%%% from Synechococcus. This remarkable variability between analogous cytochromes c6 supports the idea that different organisms utilize distinct mechanisms of photosynthetic intermolecular electron transfer.

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DIALOG(R)File 5:Biosis Previews(R)

17102983 BIOSIS NO.: 200300061702
Structural basis for the molecular properties of %%%cytochrome%%% %%%c6%%%.

AUTHOR: Dikiy Alexander; Carpentier Wesley; Vandenberghe Isabel; Borsari Marco; Safarov Niyaz; Dikaya Elena; Van Beeumen Jozef; Ciurli Stefano (Reprint)
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JOURNAL: Biochemistry 41 (50): p14689-14699 December 17, 2002 2002
MEDIUM: print
ISSN: 0006-2960 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: This is a thorough biochemical, spectroscopic, electrochemical, and structural study of a %%%cytochrome%%% %%%c6%%% isolated from the filamentous green alga Cladophora glomerata. The protein sequence, elucidated using chemical and mass spectrometric techniques, features 91 amino acids and the characteristic CXXCH %%%heme%%%-binding motif found in c-type cytochromes. The protein is monomeric in both oxidation forms, thereby putting in question a functional role for protein dimerization. Direct electrochemical measurements established, for the first time, the kinetic and thermodynamic data for the redox process in a %%%cytochrome%%% %%%c6%%%. In particular, the quasi-reversible and diffusion-controlled redox process is accompanied by negative enthalpy and entropy changes, resulting in an Eo' value of 0.352 V at 298 K. The pH-dependent properties of the oxidized protein, detected by UV-visible, NMR, and direct cyclic voltammetry, indicate the presence of two acid-base equilibria occurring in the acidic (pKa=4.5) and alkaline regions (pKa=9.0). NMR and electronic spectra allowed the assignment of these equilibria to deprotonation of %%%heme%%% propionate-7 and to replacement of the axial methionine with another ligand, respectively. The 1.3 ANG resolution X-ray structure of the oxidized protein, revealing a fold typical for class I cytochromes, suggests that the conserved Lys60 replaces the axial methionine at pH>9. The %%%heme%%% solvent accessibility is low, and no water molecules were found in the vicinity of the axial ligands of the %%%heme%%% Fe. A structure-based alignment of cytochromes c6, and the direct comparison of their structures, indicate a substantial degree of identity between the tertiary structures and suggest patches involved in protein-protein interaction. In particular, the surface electrostatic potential of cytochromes c6 features a hydrophobic region around the %%%heme%%% cofactor, and a backside surface rich in negative charges.

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DIALOG(R)File 5:Biosis Previews(R)

17041661 BIOSIS NO.: 200300000380
Increasing the conformational stability by replacement of %%%heme%%% axial

ligand in c-type cytochrome.
AUTHOR: Satoh Tadashi; Itoga Akito; Isogai Yasuhiro; Kurihara Masaaki; Yamada Seiji; Natori Miwa; Suzuki Noriko; Suruga Kohei; Kawachi Ryu; Arahira Masaomi; Nishio Toshiyuki; Fukazawa Chikafusa; Oku Tadatake (Reprint)
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JOURNAL: FEBS Letters 531 (3): p543-547 20 November, 2002 2002
MEDIUM: print
ISSN: 0014-5793
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: To investigate the role of the %%%heme%%% axial ligand in the conformational stability of c-type cytochrome, we constructed M58C and M58H mutants of the red alga Porphyra yezoensis %%%cytochrome%%% %%%c6%%% in which the sixth %%%heme%%% iron ligand (Met58) was replaced with Cys and His residues, respectively. The Gibbs free energy change for unfolding of the M58H mutant in water (DELTAGdegreeunf =1.48 kcal/mol) was lower than that of the wild-type (2.43 kcal/mol), possibly due to the steric effects of the mutation on the apoprotein structure. On the other hand, the M58C mutant exhibited a DELTAGdegreeunf of 5.45 kcal/mol, a significant increase by 3.02 kcal/mol compared with that of wild-type. This increase was possibly responsible for the sixth %%%heme%%% axial bond of M58C mutant being more stable than that of wild-type according to the %%%heme%%%-bound denaturation curve. Based on these observations, we propose that the sixth %%%heme%%% axial ligand is an important key to determine the conformational stability of c-type cytochromes, and the sixth Cys %%%heme%%% ligand will give stabilizing effects.

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DIALOG(R)File 5:Biosis Previews(R)

16285329 BIOSIS NO.: 200100457168
Structures of cytochrome c-549 and %%%cytochrome%%% %%%c6%%% from the cyanobacterium Arthrospira maxima
AUTHOR: Sawaya Michael R; Krogmann David W; Serag Ahmed; Ho Kwok Ki; Yeates Todd O; Kerfeld Cheryl A (Reprint)
AUTHOR ADDRESS: Molecular Biology Institute, University of California, Los Angeles, Los Angeles, CA, 90095-1570, USA**USA
JOURNAL: Biochemistry 40 (31): p9215-9225 August 7, 2001 2001
MEDIUM: print
ISSN: 0006-2960
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: %%%Cytochrome%%% %%%c6%%% and cytochrome c-549 are small (89 and 130 amino acids, respectively) monoheme cytochromes that function in photosynthesis. They appear to have descended relatively recently from the same ancestral gene but have diverged to carry out very different functional roles, underscored by the large difference between their

midpoint potentials of nearly 600 mV. We have determined the X-ray crystal structures of both proteins isolated from the cyanobacterium Arthrospira maxima. The two structures are remarkably similar, superimposing on backbone atoms with an rmsd of 0.7 ANG. Comparison of the two structures suggests that differences in solvent exposure of the %%%heme%%% and the electrostatic environment of the %%%heme%%% propionates, as well as in %%%heme%%% iron ligation, are the main determinants of midpoint potential in the two proteins. In addition, the crystal packing of both A. maxima cytochrome c-549 and %%%cytochrome%%% %%%c6%%% suggests that the proteins oligomerize. Finally, the cytochrome c-549 dimer we observe can be readily fit into the recently described model of cyanobacterial photosystem II.

16111727 BIOSIS NO.: 200100283566
A single arginyl residue in plastocyanin and in %%%cytochrome%%% %%%c6%%% from the cyanobacterium Anabaena sp. PCC 7119 is required for efficient reduction of photosystem I
AUTHOR: Molina-Heredia Fernando P; Hervas Manuel; Navarro Jose A; De la Rosa Miguel A (Reprint)
AUTHOR ADDRESS: Centro de Investigaciones Cientificas Isla de la Cartuja, Instituto de Bioquimica Vegetal y Fotosintesis, Universidad de Sevilla y Consejo Superior de Investigaciones Cientificas, Americo Vespucio s/n, 41092, Sevilla, Spain**Spain
JOURNAL: Journal of Biological Chemistry 276 (1): p601-605 January 5, 2001 2001
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Positively charged plastocyanin from Anabaena sp. PCC 7119 was investigated by site-directed mutagenesis. The reactivity of its mutants toward photosystem I was analyzed by laser flash spectroscopy. Replacement of arginine at position 88, which is adjacent to the copper ligand His-87, by glutamine and, in particular, by glutamate makes plastocyanin reduce its availability for transferring electrons to photosystem I. Such a residue in the copper protein thus appears to be isofunctional with Arg-64 (which is close to the %%%heme%%% group) in %%%cytochrome%%% %%%c6%%% from Anabaena (Molina-Heredia, F. P., Diaz-Quintana, A., Hervas, M., Navarro, J. A., and De la Rosa, M. A. (1999) J. Biol. Chem. 274, 33565-33570) and Synechocystis (De la Cerda, B., Diaz-Quintana, A., Navarro, J. A., Hervas, M., and De la Rosa, M. A. (1999) J. Biol. Chem. 274, 13292-13297). Other mutations concern specific residues of plastocyanin either at its positively charged east face (D49K, H57A, H57E, K58A, K58E, Y83A, and Y83F) or at its north hydrophobic pole (L12A, K33A, and K33E). Mutations altering the surface electrostatic potential distribution allow the copper protein to modulate its kinetic efficiency: the more positively charged the interaction site, the higher the rate constant. Whereas replacement of Tyr-83 by either alanine or phenylalanine has no effect on the kinetics of photosystem I reduction, Leu-12 and Lys-33 are essential for the reactivity of

plastocyanin.

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DIALOG(R)File 5:Biosis Previews(R)

15877512 BIOSIS NO.: 200100049351
Structure of %%%cytochrome%%% %%%c6%%% from the red alga Porphyra yezoensis at 1.57 ANG resolution
AUTHOR: Yamada Seiji; Park Sam-Yong; Shimizu Hideaki; Koshizuka Yasutaka; Kadokura Kazunari; Satoh Tadashi; Suruga Kohei; Ogawa Masahiro; Isogai Yasuhiro; Nishio Toshiyuki; Shiro Yoshitsugu; Oku Tadatake (Reprint)
AUTHOR ADDRESS: Department of Biological Chemistry, College of Bioresource Sciences, Nihon University, 1866 Kameino, Fujisawa, Kanagawa, 252-8510, Japan**Japan
JOURNAL: Acta Crystallographica Section D Biological Crystallography 56 (12): p1577-1582 December, 2000 2000
MEDIUM: print
ISSN: 0907-4449
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The crystal structure of %%%cytochrome%%% %%%c6%%% from the red alga Porphyra yezoensis has been determined at 1.57 ANG resolution. The crystal is tetragonal and belongs to space group P43212, with unit-cell parameters a = b = 49.26 (3), c = 83.45 (4) ANG and one molecule per asymmetric unit. The structure was solved by the molecular-replacement method and refined with X-PLOR to an R factor of 19.9% and a free R factor of 25.4%. The overall structure of %%%cytochrome%%% %%%c6%%% follows the topology of class I c-type cytochromes in which the %%%heme%%% prosthetic group covalently binds to Cys14 and Cys17, and the iron has an octahedral coordination with His18 and Met58 as the axial ligands. The sequence and the structure of the eukaryotic red algal %%%cytochrome%%% %%%c6%%% are very similar to those of a prokaryotic cyanobacterial %%%cytochrome%%% %%%c6%%% rather than those of eukaryotic green algal c6 cytochromes.

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DIALOG(R)File 5:Biosis Previews(R)

15323815 BIOSIS NO.: 200000042128
Site-directed mutagenesis of %%%cytochrome%%% %%%c6%%% from Anabaena species PCC 7119: Identification of surface residues of the hemeprotein involved in photosystem I reduction
AUTHOR: Molina-Heredia Fernando P; Diaz-Quintana Antonio; Hervas Manuel; Navarro Jose A; De la Rosa Miguel A (Reprint)
AUTHOR ADDRESS: Consejo Superior de Investigaciones Cientificas, Instituto de Bioquimica Vegetal y Fotosintesis, Universidad de Sevilla, Americo Vespucio s/n, Centro Isla de la Cartuja, 41092, Sevilla, Spain**Spain
JOURNAL: Journal of Biological Chemistry 274 (47): p33565-33570 Nov. 19, 1999 1999
MEDIUM: print
ISSN: 0021-9258

DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A number of surface residues of %%%cytochrome%%% %%%c6%%% from the cyanobacterium Anabaena sp. PCC 7119 have been modified by site-directed mutagenesis. Changes were made in six amino acids, two near the %%%heme%%% group (Val-25 and Lys-29) and four in the positively charged patch (Lys-62, Arg-64, Lys-66, and Asp-72). The reactivity of mutants toward the membrane-anchored complex photosystem I was analyzed by laser flash absorption spectroscopy. The experimental results indicate that %%%cytochrome%%% %%%c6%%% possesses two areas involved in the redox interaction with photosystem I: 1) a positively charged patch that may drive its electrostatic attractive movement toward photosystem I to form a transient complex and 2) a hydrophobic region at the edge of the %%%heme%%% pocket that may provide the contact surface for the transfer of electrons to P700. The isofunctionality of these two areas with those found in plastocyanin (which acts as an alternative electron carrier playing the same role as %%%cytochrome%%% %%%c6%%%) are evident.

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DIALOG(R)File 5:Biosis Previews(R)

15249038 BIOSIS NO.: 199900508698
Extinction coefficients and midpoint potentials of %%%cytochrome%%% %%%c6%%% from the cyanobacteria Arthrospira maxima, Microcystis aeruginosa, and Synechocystis 6803
AUTHOR: Cho Yoon Shin; Wang Qing Jun; Krogmann David; Whitmarsh John (Reprint)
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JOURNAL: Biochimica et Biophysica Acta 1413 (2): p92-97 Oct. 6, 1999 1999
MEDIUM: print
ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: %%%Cytochrome%%% %%%c6%%% is a soluble %%%heme%%% protein that serves as a photosynthetic electron transport component in cyanobacteria and algae, carrying electrons from the cytochrome bf complex to photosystem I. The rapid accumulation of %%%cytochrome%%% %%%c6%%% sequence data from a wide range of species, combined with significant advances in determining high resolution three-dimensional structures, provides a powerful database for investigating the relationship between structure and function. The fact that the gene encoding %%%cytochrome%%% %%%c6%%% can be readily modified in a number of species adds to the usefulness of %%%cytochrome%%% %%%c6%%% as a tool for comparative analysis. Efforts to relate %%%cytochrome%%% %%%c6%%% sequence information to structure, and structural information to function depend on knowledge of the physical and thermodynamic properties of the cytochrome from different species. To this end we have determined the optical extinction coefficient, the oxidation/reduction midpoint potential, and the pH dependence of themidpoint potential of %%%cytochrome%%% %%%c6%%% isolated from three cyanobacteria, Arthrospira

maxima, Microcystis aeruginosa, and Synechocystis 6803.

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DIALOG(R)File 5:Biosis Previews(R)

15163785 BIOSIS NO.: 199900423445
Amino acid sequence, crystallization and structure determination of reduced and oxidized %%%cytochrome%%% %%%c6%%% from the green alga Scenedesmus obliquus
AUTHOR: Schnackenberg Jorg (Reprint); Than Manuel E (Reprint); Mann Karlheinz; Wiegand Georg; Huber Robert; Reuter Wolfgang
AUTHOR ADDRESS: National Institute of Bioscience and Human Technology, 1-1, Higashi, Tsukuba, Ibaraki, 305-0046, Japan**Japan
JOURNAL: Journal of Molecular Biology 290 (5): p1019-1030 July 30, 1999 1999
MEDIUM: print
ISSN: 0022-2836
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: %%%Cytochrome%%% %%%c6%%% from the unicellular green alga Scenedesmus obliquus was sequenced, crystallized in its reduced and oxidized state and the three-dimensional structure of the protein in both redox states was determined by X-ray crystallography. Reduced %%%cytochrome%%% %%%c6%%% crystallized as a monomer in the space group P21212, whereas the oxidized protein crystallized as a dimer in the space group P3121. The structures were solved by molecular replacement and refined to 1.9 and 2.0 ANG, respectively. Comparison of the structures of both redox states revealed only slight differences on the protein surface, whereas a distortion along the axis between the %%%heme%%% iron and its coordinating Met61 residue was observed. No redox-dependent movement of internal water molecules could be detected. The high degree of similarity of the surfaces and charge distributions of both redox states, as well as the dimerization of %%%cytochrome%%% %%%c6%%% as observed in the oxidized crystal, is discussed with respect toits biological relevance and its implications for the reaction mechanisms between %%%cytochrome%%% %%%c6%%% and its redox partners. The dimer of oxidized %%%cytochrome%%% %%%c6%%% may represent a molecular structure occurring in a binary complex with cytochrome b6f. This assembly might be required for the correct orientation of %%%cytochrome%%% %%%c6%%% with respect to its redox partner cytochrome b6f, facilitating the electron transfer within the complex. If the dimerization is not redox-dependent in vivo, the almost identical surfaces of both redox states do not support a long range differentiation between reduced and oxidized cyt c6, i.e. a random collision model for the formation of an electron transfer complex must be assumed.

4/7/20
DIALOG(R)File 5:Biosis Previews(R)

15038830 BIOSIS NO.: 199900298490
%%%Cytochrome%%% %%%c6%%% isolated from the marine diatom Thalassiosira

weissflogii
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JOURNAL: Phytochemistry (Oxford) 51 (1): p1-4 May, 1999 1999
MEDIUM: print
ISSN: 0031-9422
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A soluble monoheme c-type %%%cytochrome%%% %%%c6%%% was isolated from the marine diatom Thalassiosira weissflogii. The isolated protein shows an apparent molecular weight of 13 kDa and an isoelectric point of 3.6 in the ferric form and 3.8 in the ferrous form. The visible spectrum of the reduced %%%cytochrome%%% %%%c6%%% is typical of a c-type %%%heme%%% protein, with maxima at 273, 416 (gamma-peak) and 553 nm (alpha-peak). The %%%cytochrome%%% %%%c6%%% isolated from T. weissflogii contains phosphoserine in its sequence. No plastocyanin was detected in the soluble extracts and no cross-reactivity was found with antibodies raised against %%%cytochrome%%% %%%c6%%% or plastocyanin from Chlorella fusca and Anabaena PCC 7119.

4/7/21
DIALOG(R)File 5:Biosis Previews(R)

14988033 BIOSIS NO.: 199900247693
Site-directed mutagenesis of %%%cytochrome%%% %%%c6%%% from Synechocystis sp. PCC 6803: The %%%heme%%% protein possesses a negatively charged area that may be isofunctional with the acidic patch of plastocyanin
AUTHOR: De la Cerda Berta; Diaz-Quintana Antonio; Navarro Jose A; Hervas Manuel; De la Rosa Miguel A (Reprint)
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JOURNAL: Journal of Biological Chemistry 274 (19): p13292-13297 May 7, 1999 1999
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: This paper reports the first site-directed mutagenesis analysis of any %%%cytochrome%%% %%%c6%%%, a %%%heme%%% protein that performs the same function as the copper-protein plastocyanin in the electron transport chain of photosynthetic organisms. Photosystem I reduction by the mutants of %%%cytochrome%%% %%%c6%%% from the cyanobacterium Synechocystis sp. PCC 6803 has been studied by laser flash absorption spectroscopy. Their kinetic efficiency and thermodynamic properties have been compared with those of plastocyanin mutants from the same organism. Such a comparative study reveals that aspartates at positions 70 and 72 in %%%cytochrome%%% %%%c6%%% are located in an acidic patch that may be isofunctional with the well known "southeast" patch of plastocyanin.

Calculations of surface electrostatic potential distribution in the mutants of %%%cytochrome%%% %%%c6%%% and plastocyanin indicate that the changes in protein reactivity depend on the surface electrostatic potential pattern rather than on the net charge modification induced by mutagenesis. Phe-64, which is close to the %%%heme%%% group and may be the counterpart of Tyr-83 in plastocyanin, does not appear to be involved in the electron transfer to photosystem I. In contrast, Arg-67, which is at the edge of the %%%cytochrome%%% %%%c6%%% acidic area, seems to be crucial for the interaction with the reaction center.

4/7/22
DIALOG(R)File 5:Biosis Previews(R)

14928006 BIOSIS NO.: 199900187666
Cytochrome c550 is an essential component of the quinoprotein ethanol oxidation system in Pseudomonas aeruginosa: Cloning and sequencing of the genes encoding cytochrome c550 and an adjacent acetaldehyde dehydrogenase
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JOURNAL: Microbiology (Reading) 145 (2): p471-481 Feb., 1999 1999
MEDIUM: print
ISSN: 1350-0872
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Pseudomonas aeruginosa ATCC 17933 grown aerobically on ethanol produces a soluble cytochrome c550 together with a quinoprotein ethanol dehydrogenase. A 3.2 kb genomic DNA fragment containing the gene encoding cytochrome c550 was cloned and sequenced. Two other complete and two truncated ORFs were also identified. A truncated ORF encoding the quinoprotein ethanol dehydrogenase (exaA) was found upstream of the cytochrome c550 gene (exaB) and in reverse orientation. An ORF encoding a NAD+-dependent acetaldehyde dehydrogenase (exaC) was located downstream of the cytochrome c550 gene and in the same orientation. Another ORF showed similarity to the pqqA gene and a truncated ORF similarity to the pqqB gene, both involved in the biosynthesis of the prosthetic group PQQ. The organization of these genes was found to be different from the well-studied methanol oxidation system in methylotrophic bacteria. The deduced amino acid sequence of cytochrome c550 from P. aeruginosa showed some similarity to %%%cytochrome%%% %%%c6%%% of the alga Chlamydomonas reinhardtii and the haem domain of quinohaemoprotein alcohol dehydrogenases of acetic acid bacteria, but no similarity to the soluble cytochrome cL of the quinoprotein methanol oxidation system of methylotrophs could be detected. A mutant of P. aeruginosa with an interrupted cytochrome c550 gene was unable to grow on ethanol, which proves that cytochrome c550 is an essential component of the ethanol oxidation system in this organism.

4/7/23
DIALOG(R)File 5:Biosis Previews(R)

14554640 BIOSIS NO.: 199800348887
A novel pathway for cytochromes c biogenesis in chloroplasts
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JOURNAL: Biochimica et Biophysica Acta 1365 (1-2): p309-318 June 10, 1998 1998
MEDIUM: print
ISSN: 0006-3002
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The cytochromes c are a useful model for the study of the pathways and mechanisms of assembly of the cofactor-containing components of energy transducing membranes. Genetic analyses have identified proteins that are required for the assembly of c-type cytochromes in mitochondria, bacteria and chloroplasts. The components of the pathway operating in fungal and animal mitochondria, i.e. the cytochrome (cyt) c and c1 %%%heme%%% lyases in the intermembrane space, were identified over a decade ago through the study of cytochrome deficiencies in Neurospora crassa and Saccharomyces cerevisiae. More recently, a large number of membrane or membrane-associated components were identified in various alpha- and gamma-proteobacteria as c-type cytochrome assembly factors; they comprise an assembly pathway that is evolutionarily and mechanistically distinct from that in fungal and animal mitochondria. The components function not only in the lyase reaction but also in the delivery and maintenance of the substrates in a state that is suitable for reaction in the bacterial periplasm. Yet a third pathway is required for cytochrome maturation in chloroplasts. Genetic analyses of Chlamydomonas reinhardtii ccs mutants, which are pleiotropically deficient in both the membrane-anchored cytochrome and the soluble %%%cytochrome%%% %%%c6%%%, revealed a minimum of six loci, plastid ccsA and nuclear CCS1 through CCS5, that are required for the conversion of the chloroplast apocytochromes to their respective holo forms. Sequence analysis of the cloned ccsA and Ccs1 genes indicates that the predicted protein products are integral membrane proteins with homologues in cyanobacteria, some gram-positive bacteria (Bacillus subtilis, Mycobacterium spp.), beta-proteobacteria (Neisseria spp.) and an epsilon-proteobacterium (Helicobacter pylori). CcsA and CcsI require each other for accumulation in vivo and are therefore proposed to function in a complex, possibly with the products of some of the other CCS loci. A tryptophan-rich motif, which has been proposed to represent a %%%heme%%% binding site in bacterial cytochrome biogenesis proteins (CcmC and CcmF), is functionally important in plastid CcsA. As is the case for CcmC and CcmF, the tryptophan-rich sequence is predicted to occur in a loop on the p-side of the membrane, where the %%%heme%%% attachment reaction occurs. Conserved histidine residues in the CcsA and Ccs1 may serve as ligands to the %%%heme%%% iron. A multiple alignment of the tryptophan-rich regions of the CcsA-, CcmC- and CcmF-like sequences in the genome databases indicates that they represent three different families.

14472435 BIOSIS NO.: 199800266682
Protein folding and protein evolution: Common folding nucleus in different subfamilies of c-type cytochromes?
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JOURNAL: Journal of Molecular Biology 278 (3): p655-666 May 8, 1998 1998
MEDIUM: print
ISSN: 0022-2836
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Amino acid sequences of seven subfamilies of cytochromes c (mitochondrial cytochromes c, c1; chloroplast cytochromes C6, cf; bacterial cytochromes C2, C550, C551; in total 164 sequences) have been compared. Despite extensive homology within eukaryotic subfamilies, homology between different subfamilies is very weak. Other than the three %%%heme%%%-binding residues (Cys13, Cys14, His18, in numeration of horse cytochrome c) there are only four positions which are conserved in all subfamiles: Gly/Ala6, Phe/Tyr10, Leu/Val/Phe94 and Tyr/Trp/Phe97. In all 17 cytochromes c with known 3D-structures, these residues form a network of conserved contacts (6-94, 6-97, 10-94, 10-97 and 94-97). Especially strong is the contact between aromatic groups in positions 10 and 97, which corresponds to 13 interatomic contacts. As residues 6, 10 and residues 94, 97 are in (i, i + 4) and (i, i + 3) positions in the N and C-terminal helices, respectively, the above mentioned system of conserved contacts consists mainly of contacts between one turn of N-terminal helix and one turn of C-terminal helix. The importance of the contacts between interfaces of these helices has been confirmed by the existence of these contacts in both equilibrium and kinetic molten globule-like folding intermediates, as well as by mutational evidence that these contacts are involved in tight packing between the N and C-helices. Since these four residues are not involved in %%%heme%%% binding and have no other apparent functional role, their conservation in highly diverged cytochromes c suggests that they are of a critical importance for protein folding. The author assumes that they are involved in a common folding nucleus of all subfamilies of c-type cytochromes.

4/7/25
DIALOG(R)File 5:Biosis Previews(R)

14377191 BIOSIS NO.: 199800171438
Purification and characterization of %%%cytochrome%%% %%%c6%%% from the unicellular green alga Scenedesmus obliquus
AUTHOR: Wuenschiers Roebbe; Zinn Thomas; Linder Dietmar; Schulz Ruediger (Reprint)
AUTHOR ADDRESS: Fachbereich Biol./Botanik, Philipps-Univ., Karl-von-Frisch-Str., D-35032 Marburg, Germany**Germany
JOURNAL: Zeitschrift fuer Naturforschung Section C Journal of Biosciences 52 (11-12): p740-746 Nov.-Dec., 1997 1997
MEDIUM: print
ISSN: 0939-5075
DOCUMENT TYPE: Article

RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Purification of a soluble %%%cytochrome%%% %%%c6%%% from the unicellular green alga Scenedesmus obliquus by a simple and rapid method is described. The purification procedure includes ammonium sulfate precipitation and non-denaturating PAGE. The N-terminal sequence of the first 20 amino acids was determined and shows 85% similarity and 75% identity to the sequence of %%%cytochrome%%% %%%c6%%% from the green alga Monoraphidium braunii. The ferrocytochrome shows typical UV/VIS absorption peaks at 552.9, 521.9 and 415.7 nm. The apparent molecular mass was estimated to be 12 kDa by SDS-PAGE. EPR-spectroscopy at 20K shows resonances indicative for two distinct low-spin %%%heme%%% forms.

4/7/26
DIALOG(R)File 5:Biosis Previews(R)

14341735 BIOSIS NO.: 199800135982
Genetic analysis of chloroplast c-type cytochrome assembly in Chlamydomonas reinhardtii: One chloroplast locus and at least four nuclear loci are required for %%%heme%%% attachment
AUTHOR: Xie Zhiyi; Culler Duane; Dreyfuss Beth Welty; Kuras Richard; Wollman Francis-Andre; Girard-Bascou Jacqueline; Merchant Sabeeha (Reprint)
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JOURNAL: Genetics 148 (2): p681-692 Feb., 1998 1998
MEDIUM: print
ISSN: 0016-6731
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Chloroplasts contain up to two c-type cytochromes, membrane-anchored cytochrome f and soluble %%%cytochrome%%% %%%c6%%%. To elucidate the post-translational events required for their assembly, acetate-requiring mutants of Chlamydomonas reinhardtii that have combined deficiencies in both plastid-encoded cytochrome f and nucleus-encoded %%%cytochrome%%% %%%c6%%% have been identified and analyzed. For strains ct34 and ct59, where the phenotype displays uniparental inheritance, the mutations were localized to the chloroplast ccsA gene, which was shown previously to be required for %%%heme%%% attachment to chloroplast apocytochromes. The mutations in another eight strains were localized to the nuclear genome. Complementation tests of these strains plus three previously identified strains of the same phenotype (ac206, F18, and F2D8) indicate that the 11 ccs strains define four nuclear loci, CCS1-CCS4. We conclude that the products of the CCS1-CCS4 loci are not required for translocation or processing of the preproteins but, like CcsA, they are required for the %%%heme%%% attachment step during assembly of both holocytochrome f and holocytochrome c6. The ccsA gene is transcribed in each of the nuclear mutants, but its protein product is absent in ccs1 mutants, and it appears to be degradation susceptible in ccs3 and ccs4 strains. We suggest that Ccs1 may be associated with CcsA in a multisubunit "holocytochrome c assembly complex," and we hypothesize that the products of the other CCS loci may correspond to other subunits.

4/7/27
DIALOG(R)File 5:Biosis Previews(R)

14321966 BIOSIS NO.: 199800116213
Solution structure of %%%cytochrome%%% %%%c6%%% from the thermophilic cyanobacterium Synechococcus elongatus
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JOURNAL: EMBO (European Molecular Biology Organization) Journal 17 (1): p 27-36 Jan. 2, 1998 1998
MEDIUM: print
ISSN: 0261-4189
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: %%%Cytochrome%%% %%%c6%%% is a small, soluble electron carrier between the two membrane-bound complexes cytochrome b6f and photosystem I (PSI) in oxygenic photosynthesis. We determined the solution structure of %%%cytochrome%%% %%%c6%%% from the thermophilic cyanobacterium Synechococcus elongatus by NMR spectroscopy and molecular dynamics calculations based on 1586 interresidual distance and 28 dihedral angle restraints. The overall fold exhibits four alpha-helices and a small antiparallel beta-sheet in the vicinity of Met58, one of the axial %%%heme%%% ligands. The flat hydrophobic area in this %%%cytochrome%%% %%%C6%%% is conserved in other c6 cytochromes and even in plastocyanin of higher plants. This docking region includes the site of electron transfer to PSI and possibly to the cytochrome b6f complex. The binding of %%%cytochrome%%% %%%c6%%% to PSI in green algae involves interaction of a negative patch with a positive domain of PSI. This positive domain has not been inserted at the evolutionary level of cyanobacteria, but the negatively charged surface region is already present in S. elongatus %%%cytochrome%%% %%%c6%%% and may thus have been optimized during evolution to improve the interaction with the positively charged cytochrome f. As the structure of PSI is known in S. elongatus, the reported %%%cytochrome%%% %%%c6%%% structure can provide a basis for mutagenesis studies to delineate the mechanism of electron transfer between both.

4/7/28
DIALOG(R)File 5:Biosis Previews(R)

14293754 BIOSIS NO.: 199800088001
Comparison of the physiologically equivalent proteins %%%cytochrome%%% %%%c6%%% and plastocyanin on the basis of their electrostatic potentials. Tryptophan 63 in %%%cytochrome%%% %%%c6%%% may be isofunctional with tyrosine 83 in plastocyanin
AUTHOR: Ullmann G Matthias (Reprint); Hauswald Markus; Jensen Axel; Kostic Nenad M; Knapp Ernst-Walter
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JOURNAL: Biochemistry 36 (51): p16187-16196 Dec. 23, 1997 1997
MEDIUM: print
ISSN: 0006-2960
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The blue copper protein plastocyanin and the %%%heme%%% protein %%%cytochrome%%% %%%c6%%% differ in composition and in structure but perform the same function in the photosynthetic electron-transport chain. We compare these two proteins on the basis of their electrostatic potentials in order to understand the structural basis of their functional equivalence. In the first approach, we use a monopole-dipole approximation of the electrostatic potentials to superimpose the proteins. The resulting alignment suggests that Tyr51 in %%%cytochrome%%% %%%c6%%% corresponds to Tyr83 in plastocyanin. But since Tyr51 is not conserved in all known %%%cytochrome%%% %%%c6%%% sequences, a physiological role of this residue is questionable. In a more sophisticated approach, we applied the recently-developed FAME (flexible alignment of molecule ensembles) algorithm, in which molecules are superimposed by optimizing the similarity of their electrostatic potentials with respect to the relative orientation of the molecules. On the basis of the FAME alignments of plastocyanin and %%%cytochrome%%% %%%c6%%%, we analyze the docking and the electron-transfer reactions of these two proteins with its physiological reaction partner cytochrome f. We derive functional analogies for individual amino acids in possible electron-transfer paths in the interprotein redox reactions. We identify two surface patches in %%%cytochrome%%% %%%c6%%% that may be involved in electron-transfer paths. The hydrophobic patch with the exposed %%%heme%%% edge in %%%cytochrome%%% %%%c6%%% may be equivalent to the hydrophobic patch with His87 in plastocyanin, whereas Trp63 in %%%cytochrome%%% %%%c6%%% may be equivalent to Tyr83 in plastocyanin. An aromatic amino acid is present at the position of Trp63 in all known %%%cytochrome%%% %%%c6%%% sequences. The electronic coupling between the %%%heme%%% and the copper site on the one side and several potentially important amino acid residues on the other is analyzed by the Pathways method. We have proposed recently that Lys65 of cytochrome f and Tyr83 of plastocyanin form a cation-pi system, which may be involved in a two-step mechanism of the electron-transfer reaction between these two proteins from higher plants. Now we corroborate this proposal by analyzing available amino acid sequences.

4/7/29

14063686 BIOSIS NO.: 199799697746
Reduction of photosystem I by cytochrome c-6 and plastocyanin: Molecular recognition and reaction mechanism
AUTHOR: Hervas Manuel; Navarro Jose A; De La Cerda Berta; Diaz Antonio; De La Rosa Miguel A (Reprint)
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JOURNAL: Bioelectrochemistry and Bioenergetics 42 (2): p249-254 1997 1997
ISSN: 0302-4598

DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Molecular recognition and protein-protein electron transfer reactions were studied in a model system in which two structurally different proteins (cytochrome c-6 and plastocyanin) are used alternatively to accomplish the same redox event, i.e. reduction of the photo-oxidized chlorophyll molecule P700+ in photosystem I (PSI). Laser flash photolysis kinetic analyses were carried out to obtain an understanding, from a structural and functional point of view, of how this interchange ability is accomplished, as well as to obtain increased insight into the electron transfer mechanisms. Our experimental data indicate that the mechanism of reaction of both the copper- and %%%heme%%%-proteins with PSI is similar within the same organism, but different from one organism to another, thereby suggesting convergent evolution of the two donor proteins.

4/7/30
DIALOG(R)File 5:Biosis Previews(R)

13144652 BIOSIS NO.: 199698612485
Ab initio determination of the crystal structure of cytochrome C-6 and comparison with plastocyanin
AUTHOR: Frazao C; Soares C M; Carrondo M A; Pohl E; Dauter Z; Wilson K S; Hervas M; Navarro J A; De La Rosa M A; Sheldrick G M (Reprint)
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JOURNAL: Structure (London) 3 (11): p1159-1169 1995 1995
ISSN: 0969-2126
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Background: Electron transfer between cytochrome f and photosystem I (PSI) can be accomplished by the %%%heme%%%-containing protein cytochrome c-6 or by the copper-containing protein plastocyanin. Higher plants use plastocyanin as the only electron donor to PSI, whereas most green algae and cyanobacteria can use either, with similar kinetics, depending on the copper concentration in the culture medium. Results: We report here the determination of the structure of cytochrome c-6 from the green alga Monoraphidium braunii. Synchrotron X-ray data with an effective resolution of 1.2 ANG and the presence of one iron and three sulfur atoms enabled, possibly for the first time, the determination of an unknown protein structure by ab initio methods. Anisotropic refinement was accompanied by a decrease in the 'free' R value of over 7%; the anisotropic motion is concentrated at the termini and between residues 38 and 53. The %%%heme%%% geometry is in very good agreement with a new see of %%%heme%%% distances derived from the structures of small molecules. This is probably the most precise structure of a %%%heme%%% protein to date. Conclusions: On the basis of this cytochrome c-6 structure, we have calculated potential electron transfer pathways and made comparisons with similar analyses for plastocyanin. Electron transfer between the copper redox center of plastocyanin to PSI and from cytochrome f is believed to involve two sites on the protein. In contrast, cytochrome c-6 may well

use just one electron transfer site, close to the %%%heme%%% unit, in its corresponding reactions with the same two redox partners.

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DIALOG(R)File 5:Biosis Previews(R)

12962316 BIOSIS NO.: 199598430149
The structure of chloroplast %%%cytochrome%%% %%%c6%%% and 1.9 A resolution: Evidence for functional oligomerization
AUTHOR: Kerfeld Cheryl A (Reprint); Anwar Haroon P; Interrante Robert; Merchant Sabeeha; Yeates Todd O
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JOURNAL: Journal of Molecular Biology 250 (5): p627-647 1995 1995
ISSN: 0022-2836
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The molecular structure of %%%cytochrome%%% %%%c6%%% from the green alga Chlamydomonas reinhardtii has been determined from two crystal forms and refined to 1.9 ANG resolution. The two crystal forms are likely the result of different levels of post-translational modification of the protein. This is the first report of a high-resolution structure of a chloroplast-derived class I c-type cytochrome. The overall fold is similar to that of other class I c-type cytochromes, consisting of a series of alpha-helices and turns that envelop the %%%heme%%% prosthetic group. There is also a short two-stranded anti-parallel beta-sheet in the vicinity of the methionine axial ligand to the %%%heme%%%; this region of the molecule is formed by the most highly conserved residues in c6-type cytochromes. Although class I c-type cytochromes are assumed to function as monomers, both crystal forms of %%%cytochrome%%% %%%c6%%% exhibit oligomerization about the %%%heme%%% crevice that is, in part, mediated by the short anti-parallel beta-sheet. The functional significance of this oligomerization is supported by the appearance of similar interfaces in other electron transfer couples, HPLC and light-scattering data, and is furthermore consistent with kinetic data on electron transfer reactions of c6-type cytochromes.

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DIALOG(R)File 5:Biosis Previews(R)

12819279 BIOSIS NO.: 199598287112
Cytochrome c-6 from the green alga Monoraphidium braunii. Crystallization and preliminary diffraction studies
AUTHOR: Frazao Carlos; Dias Joao M; Matias Pedro M; Romao Maria J; Carrondo Maria A (Reprint); Hervas Manuel; Navarro Jose A; De La Rosa Miguel; Sheldrick George M
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JOURNAL: Acta Crystallographica Section D Biological Crystallography 51 (2): p232-234 1995 1995

ISSN: 0907-4449
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Cytochrome c-6, a plastocyanin functionally interchangeable electron carrier between the chlorophyll molecule P700 of photosystem I and cytochrome f from cytochrome b-6f complex, has been isolated from the green alga Monoraphidium braunii and crystallized by the vapour-diffusion technique in sodium citrate. Crystals belong to space group R3, with cell dimensions a = b = 51.93 (5) and c = 80.5 (1) ANG (hexagonal axes), with one molecule per asymmetric unit. They diffract beyond 1.9 ANG under a Cu K-alpha rotating-anode source, with an anomalous signal that allows the positioning of the %%%heme%%% Fe atom in the unit cell.

4/7/33

12758474 BIOSIS NO.: 199598226307

Coordinate expression of coproporphyrinogen oxidase and %%%cytochrome%%% %%%c6%%% in the green alga Chlamydomonas reinhardtii in responses to changes in copper availability

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JOURNAL: EMBO (European Molecular Biology Organization) Journal 14 (5): p 857-865 1995 1995
ISSN: 0261-4189
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: To maintain photosynthetic competence under copper-deficient conditions, the green alga Chlamydomonas reinhardtii substitutes a %%%heme%%% protein (%%%cytochrome%%% %%%c6%%%) for an otherwise essential copper protein, viz. plastocyanin. Here, we report that the gene encoding coproporphyrinogen oxidase, an enzyme in the %%%heme%%% biosynthetic pathway, is coordinately expressed with %%%cytochrome%%% %%%c6%%% in response to change; in copper availability. We have purified coproporphyrinogen oxidase from copper-deficient C. reinhardtii cells, and have cloned a cDNA fragment which encodes it. Northern hybridization analysis confirmed that the protein is nuclear-encoded and that, like %%%cytochrome%%% %%%c6%%%, its expression is regulated by copper at the level of mRNA accumulation. The copper-responsive expression of coproporphyrinogen oxidase parallels %%%cytochrome%%% %%%c6%%% expression exactly. Specifically the copper-sensing range and metal selectivity of the regulatory components, as well as the time course of the responses, are identical. Hence, we propose that the expression of these two proteins is controlled by the same metalloregulatory mechanism. Our findings represent a novel metalloregulatory response in which the synthesis of one redox cofactor (%%%heme%%%) is controlled by the availability of another (Cu).

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12709110 BIOSIS NO.: 199598176943
Biosynthesis of cytochrome f in Chlamydomonas reinhardtii: Analysis of the pathway in gabaculine-treated cells and in the %%%heme%%% attachment mutant B6
AUTHOR: Howe Gregg; Mets Laurens; Merchant Sabeeha (Reprint)
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JOURNAL: Molecular and General Genetics 246 (2): p156-165 1995 1995
ISSN: 0026-8925
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Chlamydomonas reinhardtii uses two c-type cytochromes for photosynthetic electron transfer: the thylakoid membrane-bound cytochrome f of the cytochrome b6f complex and the soluble %%%cytochrome%%% %%%c6%%% . Previously, a class of photosynthesis-minus, acetate-requiring mutants was identified which were deficient in both c-type cytochromes, and biochemical analyses of %%%cytochrome%%% %%%c6%%% biosynthesis in these strains indicated that they were each blocked at the step of %%%heme%%% attachment to apocytochrome c6. In order to demonstrate that the deficiency in cytochrome f results from the same biochemical and genetic defect, cytochrome f biosynthesis was examined in the B6 mutant (a representative of this phenotypic class) and in spontaneous suppressor strains derived from B6. Pulse-radiolabeling experiments show that B6 synthesizes a form of cytochrome f that is rapidly degraded in vivo. This polypeptide is membrane associated and migrates with an electrophoretic mobility identical to that of standard apocytochrome f produced in vitro but slightly greater than that of standard holocytochrome f produced in vivo by wild-type cells. These findings suggest that the B6 strain is unable to convert apocytochrome f to holocytochrome f and that apocytochrome f is unstable in vivo. In the suppressed strains, accumulation of both holocytochrome f and holocytochrome c6 is restored. One suppressor mutation (strain B6R) displays uniparental inheritance whereas another (B6T3) displays Mendelian inheritance. In both cases, the three phenotypes, photosynthesis-plus, b6f+ and cyt c6+ co-segregate in genetic crosses. This study therefore confirms that the dual cyt b6f-/cytc6- deficiency in B6 results from a single mutation that affects a step in holocytochrome formation that is common to the biosynthetic pathways of both plastidic c-type cytochromes. The study also confirms that pre-apocytochrome f synthesis, processing and association with the membrane is not dependent on %%%heme%%% attachment. Synthesis of cytochrome f does, however, appear to be dependent on %%%heme%%% availability. In cells depleted of tetrapyrrole pathway intermediates by gabaculine treatment, cytochrome f synthesis was significantly reduced. Since gabaculine treatment did not affect the stability of cytochrome f nor the accumulation of cytochrome f-encoding transcripts, the reduction is attributed to post-transcriptional regulation of pre-apocytochrome f synthesis via a pathway that is sensitive to the availability of %%%heme%%% or a tetrapyrrole pathway intermediate.

12388605 BIOSIS NO.: 199497409890
Cloning and correct expression in E. coli of the petJ gene encoding cytochrome c-6 from Synechocystis 6803
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JOURNAL: FEBS (Federation of European Biochemical Societies) Letters 347 (2-3): p173-177 1994 1994
ISSN: 0014-5793
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Cytochrome c-6 from the cyanobacterium Synechocystis 6803 has been isolated and purified to electrophoretic homogeneity. The gene coding for such a %%%heme%%% protein (petJ) has been cloned and properly expressed in E. coli. This procedure yields a protein preparation completely identical to that obtained from the cyanobacterial cells. The N-terminal amino acid sequences of cytochrome c-6 synthesized in both organisms are the same, thus allowing us to conclude that the petJ gene product is correctly processed in E. coli. To the best of our knowledge, this is the first time that any cytochrome c-6 is produced in the enterobacterium. The identical physicochemical and kinetic properties of the proteins isolated from both sources confirm that expression of the petJ gene in E. coli is an adequate tool to address the study of Synechocystis cytochrome c-6 by site-directed mutagenesis in a parallel way to that carried out with plastocyanin from the same organism.

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DIALOG(R)File 5:Biosis Previews(R)

12176023 BIOSIS NO.: 199497197308
Laser flash kinetic analysis of Synechocystis PCC 6803 cytochrome C-6 and plastocyanin oxidation by photosystem I
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JOURNAL: Biochimica et Biophysica Acta 1184 (2-3): p235-241 1994 1994
ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Laser flash absorption spectroscopy has been used to investigate the kinetics of electron transfer from reduced cytochrome c-6 and plastocyanin to photooxidized P700 in Photosystem I (PS I) particles from the cyanobacterium Synechocystis PCC 6803. Data analysis yields second-order rate constants of 1.3 cntdot 10-7 M-1 s-1 and 1.0 cntdot 10-7 M-1 s-1 for the %%%heme%%%- and copper-proteins, respectively. With the two donor proteins, the observed rate constants (k-obs) present a linear protein-concentration dependence, thus suggesting an apparent

one-step bimolecular collisional mechanism. At neutral pH, the k-obs values monotonically increase with increasing NaCl or MgCl-2 concentration, which is ascribed to the involvement of repulsive electrostatic interactions between the donor proteins and PS I. The difference in the effective concentration at which MgCl-2 has its maximum effect as compared with that of NaCl is attributed to the specific role played by Mg-2+ ions, which could act as electrostatic bridges between negatively charged groups. At physiological mild acid pH, cytochrome c-6 is a more efficient electron donor than plastocyanin. The inversion of the NaCl and MgCl-2 effect at pH below 5 - that is, decreasing of k-obs with increasing ionic strength - is interpreted as arising from the involvement of attractive ionic interactions at pH lower than the isoelectric point of the donor proteins. Some evolutive aspects on the mechanism of electron donation to PS I are discussed.

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DIALOG(R)File 5:Biosis Previews(R)

12175948 BIOSIS NO.: 199497197233
Role of %%%heme%%% in the biosynthesis of cytochrome c-6
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JOURNAL: Journal of Biological Chemistry 269 (8): p5824-5832 1994 1994
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Cytochrome c-6, a nuclear-encoded protein, is synthesized in the cytoplasm in a precursor form (pre-apocytochrome c-6). Time course radiolabeling experiments support the model that the pre-protein is the substrate for a lumen-targeting post-translational pathway which includes two proteolytic cleavage events and the covalent attachment of %%%heme%%% to cysteinyl thiols on the polypeptide. Cell fractionation studies indicate that the fully processed protein fractionates with other soluble proteins, whereas the precursor and intermediate forms appear to be membrane-associated. To determine whether either of the processing steps is influenced by %%%heme%%% attachment, the biosynthetic pathway was examined 1) in a Chlamydomonas reinhardtii mutant (B6) that is defective in the %%%heme%%% attachment step and 2) in wild-type cells treated with gabaculine, an inhibitor of %%%heme%%% synthesis. In vivo radiolabeling experiments with the B6 mutant showed that a defect in %%%heme%%% attachment affects neither the synthesis of the pre-apoprotein nor its processing to the mature apoform to any significant extent, supporting the notion that %%%heme%%% attachment and processing are not obligatorily coupled in this pathway. A similar conclusion is reached from examination of cytochrome c-6 synthesis in gabaculine-treated cells where inhibition of %%%heme%%% attachment did not prevent either of the two processing steps. The fully processed apoprotein is a suitable substrate for %%%heme%%% attachment in vivo, since the apoprotein was indeed converted to holoprotein in gabaculine-treated cells, albeit more slowly than in untreated cells. Despite the lack of effect of gabaculine treatment on the accumulation of cytochrome c-6-encoding messages, the amount of holocytochrome c-6 precursors synthesized during a brief labeling period

is 4-7-fold less than in untreated cells, suggesting that synthesis of the polypeptide may be coupled to %%%heme%%% availability by a control mechanism operating at the translational level.

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11952230 BIOSIS NO.: 199396116646
Cytochrome c-6 from Monoraphidium braunii: A cytochrome with an unusual %%%heme%%% axial coordination
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JOURNAL: European Journal of Biochemistry 216 (1): p329-341 1993
ISSN: 0014-2956
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A soluble monoheme c-type cytochrome (cytochrome c-6) has been isolated from the green alga Monoraphidium braunii. It has a molecular mass of 9.3 kDa, an isoelectric point of 3.6 and a reduction potential of 358 mV at pH 7. The determined amino acid sequence allows its classification as a class-I c-type cytochrome. The ferric and ferrous cytochrome forms and their pH equilibria have been studied using 1H-NMR, ultraviolet/visible, EPR and Moessbauer spectroscopies. The pH equilibria are complex, several pK-a values and pH-dependent forms being observed. The amino acid sequence, the reduction-potential value and the visible and NMR spectroscopies data in the pH range 4-9 indicate that the %%%heme%%% iron has a methionine-histidine axial coordination. However, the EPR and Moessbauer data obtained for the ferricytochrome show that in this pH range two distinct forms are present: form I, g-z = 3.27, g-y = 2.05 and g-x = 1.05; form II, g-z = 2.95, g-y = 2.29 and g-x = 1.43. While form I has crystal-field parameters typical of a methionine-histidine coordination, those associated with form II would suggest a histidine-histidine axial ligation. This possibility was extensively analyzed by spectroscopic methods and by chemical modification of a histidine residue. It was concluded that form II actually corresponds to an unusual type of methionine-histidine axial coordination. Straightforward examples of this type of coordination have recently been found in other c-type hemeproteins (Teixeira, M., Campos, A. P., Aguiar, A. P, Costa, H. S., Santos, H., Turner, D. L. and Xavier, A. V. (1993) FEBS Lett. 317, 233-236), corroborating our proposal. Since both forms, with very distinct crystal-field parameters, are shown to have the same reduction potential, it may be concluded that the axial and rhombic distortions of the %%%heme%%%-iron ligand field cannot be directly correlated with the %%%heme%%%-reduction potential. The pH-dependence studies have also shown that the form I and form II are interconvertible, with pK-a apprxeq 5. To establish a possible physiological significance for this process, in particular for the interaction of the cytochrome with the membrane-bound electron-transfer complexes b-6f and photosystem I, the effect of surfactants on the spectroscopic characteristics of cytochrome c-6 has been studied.

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DIALOG(R)File 5:Biosis Previews(R)

11383086 BIOSIS NO.: 199294084927
THE BIOSYNTHESIS OF MEMBRANE AND SOLUBLE PLASTIDIC C-TYPE CYTOCHROMES OF CHLAMYDOMONAS-REINHARDTII IS DEPENDENT ON MULTIPLE COMMON GENE PRODUCTS
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JOURNAL: EMBO (European Molecular Biology Organization) Journal 11 (8): p 2789-2801 1992
ISSN: 0261-4189
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: %%%Cytochrome%%% %%%c6%%% functions in the thylakoid lumen to catalyze electron transfer from reduced cytochrome f of the cytochrome b6f complex to P700+ of photosystem I. The biogenesis of mature cyt c6 from cytosolically translated pre-apocytochrome c6 involves numerous post-translationsl modifications including the proteolytic removal of a transit sequence and the covalent attachment of %%%heme%%% to two cysteinyl thiols on the apoprotein. Here, we report on the characterization of a previously unrecognized class of non-allelic mutants of Chlamydomonas reinhardtii that are blocked at the conversion of apocyt c6 to holocyt c6. The mutants are acetate requiring since they are also deficient in cyt f, cyt b and the Rieske FeS protein. Pulse-chase studies indicate that %%%heme%%% attachment is not required for the two-step processing of pre-apocytochrome c6 to apocyt c6, but is required for the stability of the mature protein. This is in contrast to the biosynthesis of mitochondrial cyt c1 where %%%heme%%% attachment is required for the second processing step. We propose that the assembly of both holocytochrome c6 and the cytochrome b6f complex are dependent on common gene products, possibly those involved in %%%heme%%% delivery or metabolism. This is the first suggestion that multiple loci are involved in the biosynthesis of both plastidic c-type cytochromes.

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DIALOG(R)File 5:Biosis Previews(R)

09103710 BIOSIS NO.: 198885072601
STUDIES ON ALGAL CYTOCHROMES VI. SOME PROPERTIES AND AMINO ACID SEQUENCE OF CYTOCHROME C-6 FROM A GREEN ALGA BRYOPSIS-MAXIMA
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JOURNAL: Journal of Biochemistry (Tokyo) 102 (5): p1251-1260 1987
ISSN: 0021-924X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A photosynthetic c-type cytochrome, %%%cytochrome%%% %%%c6%%%,

was extracted from a green alga, Bryopsis maxima, by cutting and immersing the frozen thalli in phosphate buffer, pH 7.0, and purified by acrinol treatment, ammonium sulfate fractionation, DEAE-Sephacel chromatography and Bio-Gel P-10 gel filtration. The ferrocytochrome c6 has absorption maxima at 553.5 (.alpha.), 523 (.beta.), 417 (.gamma.), 318 (.delta.), and 275 nm and the ferricytochrome at 695, 528, and 411 (.gamma.). The molecular weight was estimated to be about 10,000 from Sephadex G-75 gel filtration and sodium dodecyl sulfate (SDS)-polyacrylamide gel electrophoresis (PAGE). The midpoint redox potential for the cytochrome was determined by equilibrium titration with a ferro- and ferricyanide system to be 0.385 volt at pH 7.0. Isoelectric points for ferro- and ferricytochromes were determined by density gradient isoelectric focusing electrophoresis to be at pH 3.91 and 4.02, respectively. The complete amino acid sequence of the cytochrome was determined by Edman degradation and by carboxypeptidase digestions of the Cm-cytochrome, 6 staphylococcal protease peptides and 5 lysyl endopeptidase peptides. The cytochrome contained 88 amino acid residues, giving a molecular weight of 9,904 including 1 mol of %%%heme%%% c. The sequence is as follows:
GGDLEIGADVFTGNCAACHAGGANSVEPLKTLNKED-VTKYLDGGLSIEAITSQVRNGKGAMPAWSDRLDDEE
IDGVVAYVFKNINE-GW. A phylogenetic tree of 12 algal cytochromes c6 was constructed by comparing the amino acid differences.

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